GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 10:38:49 ; Search time 2671.52 Seconds
(without alignments)
123.504 Million cell updates/sec

Title: US-09-923-515-34
Perfect score: 20
Sequence: 1 ctggcggtgaccatgtagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description
c	1	20	100.0	39	6	I34469	I34469 Sequence 5
	2	14.2	71.0	42	6	AX044129	AX044129 Sequence
c	3	14.2	71.0	50	6	AX044074	AX044074 Sequence
c	4	14.2	71.0	50	6	AX044119	AX044119 Sequence
c	5	14.2	71.0	50	6	AX044167	AX044167 Sequence
c	6	13.6	68.0	40	6	AR148823	AR148823 Sequence
c	7	13.2	66.0	28	6	AX038841	AX038841 Sequence
	8	12.8	64.0	21	6	AX052646	AX052646 Sequence
c	9	12.8	64.0	27	6	AX069478	AX069478 Sequence
c	10	12.6	63.0	48	6	AR028565	AR028565 Sequence
c	11	12.6	63.0	51	6	AX160127	AX160127 Sequence
c	12	12.4	62.0	25	6	AR090800	AR090800 Sequence
	13	12.4	62.0	39	6	AX044076	AX044076 Sequence
c	14	12.4	62.0	39	6	AX044077	AX044077 Sequence
	15	12.4	62.0	39	6	AX044121	AX044121 Sequence
c	16	12.4	62.0	39	6	AX044122	AX044122 Sequence
	17	12.4	62.0	39	6	AX044169	AX044169 Sequence
c	18	12.4	62.0	39	6	AX044170	AX044170 Sequence
c	19	12.4	62.0	56	5	XELIGHAN	M30037 X.laevis Ig
	20	12.2	61.0	17	6	I46487	I46487 Sequence 46
	21	12.2	61.0	17	6	I46488	I46488 Sequence 46
	22	12.2	61.0	17	6	I46489	I46489 Sequence 46
	23	12.2	61.0	18	6	AR092846	AR092846 Sequence
c	24	12.2	61.0	24	6	AR078736	AR078736 Sequence
c	25	12.2	61.0	42	6	AX046554	AX046554 Sequence
c	26	12.2	61.0	45	6	AR139579	AR139579 Sequence
c	27	12.2	61.0	45	6	I34855	I34855 Sequence 61
c	28	12.2	61.0	51	6	AR077557	AR077557 Sequence
	29	12.2	61.0	51	6	AX163100	AX163100 Sequence
c	30	12	60.0	21	6	AX096629	AX096629 Sequence
	31	12	60.0	23	6	AR029530	AR029530 Sequence
	32	12	60.0	23	6	AR098483	AR098483 Sequence
	33	12	60.0	23	6	I41443	I41443 Sequence 40
c	34	12	60.0	31	6	AR026959	AR026959 Sequence
c	35	12	60.0	34	6	AR034269	AR034269 Sequence
c	36	12	60.0	36	6	A91017	A91017 Sequence 14
c	37	12	60.0	36	6	E50976	E50976 Assay, rece
c	38	12	60.0	38	6	AR091866	AR091866 Sequence
	39	12	60.0	38	6	AR091867	AR091867 Sequence
	40	12	60.0	42	6	AR026357	AR026357 Sequence
c	41	12	60.0	42	6	AR026357	AR026357 Sequence
	42	12	60.0	42	6	AR026363	AR026363 Sequence
c	43	12	60.0	42	6	AR026363	AR026363 Sequence
c	44	12	60.0	44	6	AR061555	AR061555 Sequence
c	45	12	60.0	44	6	AR108454	AR108454 Sequence

ALIGNMENTS

RESULT 1
I34469/c
LOCUS I34469 39 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 5 from patent US 5597908.
ACCESSION I34469
VERSION I34469.1 GI:1825260
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Taddei-Peters,W.C. and Butler,S.M.
TITLE Immunoreactive peptides of apo(a)
JOURNAL Patent: US 5597908-A 5 28-JAN-1997;
FEATURES Location/Qualifiers
source 1..39
/organism="unknown"
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100%

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Db     23 CTGGCGGTGACCATGTAGTC 4


RESULT   2
AX044129
LOCUS       AX044129       42 bp    DNA             PAT       24-NOV-2000
DEFINITION  Sequence 29 from Patent WO0066747.
ACCESSION   AX044129
VERSION     AX044129.1  GI:11343007
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Hawkes,T.R., Warner,S.A., Andrews,C.J., Bachoo,S. and
            Pickerill,A.P.
  TITLE     Herbicide resistant plants
  JOURNAL   Patent: WO 0066747-A 29 09-NOV-2000;
            ZENECA LIMITED (GB)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="primer"
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  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 tggcggtgaccatgtagtc 20
          ||||||| |||||||  |||
Db     23 TGGCGGCGACCATGGCGTC 41


RESULT   3
AX044074/c
LOCUS       AX044074       50 bp    DNA             PAT       24-NOV-2000
DEFINITION  Sequence 29 from Patent WO0066748.
ACCESSION   AX044074
VERSION     AX044074.1  GI:11342952
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Hawkes,T.R., Warner,S.A., Andrews,C.J., Bachoo,S. and
            Pickerill,A.P.
  TITLE     Herbicide resistant plants
  JOURNAL   Patent: WO 0066748-A 29 09-NOV-2000;
            ZENECA LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="primer"
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ORIGIN


  Query Match             71.0%;  Score 14.2;  DB 6;  Length 50;
  Best Local Similarity   84.2%;  Pred. No. 3e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 tggcggtgaccatgtagtc 20
          ||||||| |||||||  |||
Db     19 TGGCGGCGACCATGGCGTC 1


RESULT   4
AX044119/c
LOCUS       AX044119       50 bp    DNA             PAT       24-NOV-2000
DEFINITION  Sequence 19 from Patent WO0066747.
ACCESSION   AX044119
VERSION     AX044119.1  GI:11342997
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Hawkes,T.R., Warner,S.A., Andrews,C.J., Bachoo,S. and
            Pickerill,A.P.
  TITLE     Herbicide resistant plants
  JOURNAL   Patent: WO 0066747-A 19 09-NOV-2000;
            ZENECA LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .50
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                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT       11 a      18 c      15 g       6 t
ORIGIN


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  Best Local Similarity   84.2%;  Pred. No. 3e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 tggcggtgaccatgtagtc 20
          ||||||| |||||||  |||
Db     19 TGGCGGCGACCATGGCGTC 1


RESULT   5
AX044167/c
LOCUS       AX044167       50 bp    DNA             PAT       24-NOV-2000
DEFINITION  Sequence 19 from Patent WO0066746.
ACCESSION   AX044167
VERSION     AX044167.1  GI:11343045
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Hawkes,T.R., Warner,S.A., Andrews,C.J., Bachoo,S. and
            Pickerill,A.P.
  TITLE     Herbicide resistant plants
  JOURNAL   Patent: WO 0066746-A 19 09-NOV-2000;
            ZENECA LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .50
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                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT       11 a      18 c      15 g       6 t
ORIGIN


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  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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          ||||||| |||||||  |||
Db     19 TGGCGGCGACCATGGCGTC 1
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RESULT   6
AR148823/c
LOCUS       AR148823       40 bp    DNA             PAT       08-AUG-2001
DEFINITION  Sequence 180 from patent US 6225451.
ACCESSION   AR148823
VERSION     AR148823.1  GI:15112913
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Ballinger,D.G., Ding,W., Wagner,S. and Hess,M.A.
  TITLE     Chromosome 11-linked coronary heart disease susceptibility gene
            CHD1
  JOURNAL   Patent: US 6225451-A 180 01-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="unknown"
BASE COUNT        8 a      13 c      10 g       9 t
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  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 ctggcggtgaccatgtagtc 20
           ||||| |||| ||||  |||
Db      34 CTGGCCGTGAACATGGCGTC 15


RESULT   7
AX038841/c
LOCUS       AX038841       28 bp    DNA             PAT       16-NOV-2000
DEFINITION  Sequence 20 from Patent WO0061792.
ACCESSION   AX038841
VERSION     AX038841.1  GI:11228166
KEYWORDS    .
SOURCE      Escherichia coli.
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Labischinski,H., Wieland,B., Broetz,H., Ehlert,K., Freiberg,C. and
            Spaltmann,F.
  TITLE     Novel essential bacterial genes and their proteins
  JOURNAL   Patent: WO 0061792-A 20 19-OCT-2000;
            LABISCHINSKI HARALD (DE) ; WIELAND BERND (DE) ; BAYER AG (DE) ;
            BROETZ HEIKE (DE) ; EHLERT KERSTIN (DE) ; FREIBERG CHRISTOPH (DE) ;
            SPALTMANN FRANK (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Escherichia coli"
                     /db_xref="taxon:562"
                     /note="Primer YGBP1A"
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  Best Local Similarity   83.3%;  Pred. No. 1e+05;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 ctggcggtgaccatgtag 18
           | ||| ||||||||||| |
Db      27 CAGGCAGTGACCATGTGG 10


RESULT   8
AX052646
LOCUS       AX052646       21 bp    DNA             PAT       12-JAN-2001
DEFINITION  Sequence 31 from Patent WO0071726.
ACCESSION   AX052646
VERSION     AX052646.1  GI:12226836
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Federspiel,M.J.
  TITLE     Methods to inhibit infectious agent transmission during
            xenotransplantation
  JOURNAL   Patent: WO 0071726-A 31 30-NOV-2000;
            Mayo Medical Ventures (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
BASE COUNT        1 a       3 c       8 g       9 t
ORIGIN


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  Best Local Similarity   87.5%;  Pred. No. 1.6e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 gcggtgaccatgtagt 19
           |||||| || ||||||
Db       5 GCGGTGTCCTTGTAGT 20


RESULT   9
AX069478/c
LOCUS       AX069478       27 bp    DNA             PAT       25-JAN-2001
DEFINITION  Sequence 142 from Patent WO0102600.
ACCESSION   AX069478
VERSION     AX069478.1  GI:12579264
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Yuan,C.S.
  TITLE     Detection of analytes using attenuated enzymes
  JOURNAL   Patent: WO 0102600-A 142 11-JAN-2001;
            GENERAL ATOMICS (US)
FEATURES             Location/Qualifiers
     source          1. .27
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                     /db_xref="taxon:32630"
                     /note="Oligonucleotide used for site-directed mutagenesis
                     of Human SAH hydrolase (Mutant K186A)"
     variation       13. .15
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ORIGIN


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  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 ctggcggtgaccatgt 16
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Db      17 CTGGCGGTGACGAAGT 2


RESULT  10
AR028565/c
LOCUS       AR028565       48 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 4 from patent US 5858724.
ACCESSION   AR028565
VERSION     AR028565.1  GI:5940538
KEYWORDS    .
SOURCE      Unknown.
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Novy,R.E. Jr., Domanico,M.J., Yaeger,K.W. and Kroeker,W.
  TITLE     Recombinant rabbit tissue factor
  JOURNAL   Patent: US 5858724-A 4 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="unknown"
BASE COUNT       16 a     11 c     12 g      9 t
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  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Db     43 CTGTCTGTGACCGTGTACT 25


RESULT  11
AX160127/c
LOCUS       AX160127       51 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 3455 from Patent WO0140521.
ACCESSION   AX160127
VERSION     AX160127.1  GI:14541458
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 3455 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
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RESULT  12
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LOCUS       AR090800       25 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 920 from patent US 5994076.
ACCESSION   AR090800
VERSION     AR090800.1  GI:10017555
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 920 30-NOV-1999;
FEATURES             Location/Qualifiers
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BASE COUNT        6 a      8 c      7 g      4 t
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  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db     23 TGGCGGTGCCCATG 10


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LOCUS       AX044076       39 bp    DNA             PAT       24-NOV-2000
DEFINITION  Sequence 31 from Patent WO0066748.
ACCESSION   AX044076
VERSION     AX044076.1  GI:11342954
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Hawkes,T.R., Warner,S.A., Andrews,C.J., Bachoo,S. and
            Pickerill,A.P.
  TITLE     Herbicide resistant plants
  JOURNAL   Patent: WO 0066748-A 31 09-NOV-2000;
            ZENECA LIMITED (GB)
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BASE COUNT        6 a     13 c     15 g      5 t
ORIGIN


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  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 tggcggtgaccatg 15
          |||||| |||||||
Db     24 TGGCGGCGACCATG 37


RESULT  14
AX044077/c
LOCUS       AX044077       39 bp    DNA             PAT       24-NOV-2000
DEFINITION  Sequence 32 from Patent WO0066748.
ACCESSION   AX044077
VERSION     AX044077.1  GI:11342955
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Hawkes,T.R., Warner,S.A., Andrews,C.J., Bachoo,S. and
            Pickerill,A.P.
  TITLE     Herbicide resistant plants
  JOURNAL   Patent: WO 0066748-A 32 09-NOV-2000;
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ORIGIN
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ACCESSION   AX044121
VERSION     AX044121.1  GI:11342999
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 39)
  AUTHORS   Hawkes,T.R., Warner,S.A., Andrews,C.J., Bachoo,S. and
            Pickerill,A.P.
  TITLE     Herbicide resistant plants
  JOURNAL   Patent: WO 0066747-A 21 09-NOV-2000;
            ZENECA LIMITED (GB)
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           |||||| |||||||
Db      24 TGGCGGCGACCATG 37


Search completed: March 13, 2002, 10:38:50
Job time: 4147 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 10:38:50 ; Search time 2671.52 Seconds
(without alignments)
123.504 Million cell updates/sec

Title: US-09-923-515-35
Perfect score: 20
Sequence: 1 tctaagtaggttgatgcttc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vi:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description
1		15	75.0	33	6	I34489	I34489 Sequence 43
2	c	13.8	69.0	54	6	AX106346	AX106346 Sequence
3	c	13.8	69.0	54	6	AX140637	AX140637 Sequence
4		13.6	68.0	59	6	AX011484	AX011484 Sequence
5		12.8	64.0	52	6	AX080760	AX080760 Sequence
6		12.6	63.0	34	6	AR012698	AR012698 Sequence
7	c	12.6	63.0	56	6	AR023824	AR023824 Sequence
8	c	12.6	63.0	56	6	I46850	I46850 Sequence 31
9	c	12.6	63.0	58	3	DROPEIS8	D12606 D.melanogas
10		12.2	61.0	29	6	E04190	E04190 linker DNA.
11		12.2	61.0	29	6	E04195	E04195 linker DNA.
12		12.2	61.0	35	6	AX167992	AX167992 Sequence
13		12	60.0	24	6	A92655	A92655 Sequence 3
14	c	12	60.0	28	6	E13871	E13871 PCR primer
15	c	12	60.0	54	6	AR134189	AR134189 Sequence
16	c	12	60.0	54	6	I38035	I38035 Sequence 10
17	c	12	60.0	54	6	I94885	I94885 Sequence 10
18	c	12	60.0	58	6	A91101	A91101 Sequence 4
19	c	11.8	59.0	39	6	AX044059	AX044059 Sequence
20	c	11.8	59.0	48	6	AX163055	AX163055 Sequence
21	c	11.8	59.0	48	6	AX163056	AX163056 Sequence
22	c	11.8	59.0	52	10	D89998	D89998 Rattus sp.
23		11.8	59.0	57	9	AF267766	AF267766 Homo sapi
24	c	11.6	58.0	28	6	AR090635	AR090635 Sequence
25		11.6	58.0	35	6	A43052	A43052 Sequence 5
26		11.6	58.0	35	6	AR047853	AR047853 Sequence
27		11.6	58.0	35	6	I16860	I16860 Sequence 5
28	c	11.6	58.0	37	6	AR107038	AR107038 Sequence
29	c	11.6	58.0	45	6	AR026954	AR026954 Sequence
30		11.6	58.0	46	6	AR124898	AR124898 Sequence
31		11.6	58.0	48	6	AR106451	AR106451 Sequence
32	c	11.6	58.0	48	6	AR106456	AR106456 Sequence
33		11.6	58.0	51	6	AX161071	AX161071 Sequence
34		11.6	58.0	51	6	AX161072	AX161072 Sequence
35		11.6	58.0	51	6	AX163192	AX163192 Sequence
36		11.6	58.0	56	8	CNS0190S	AL111043 Botrytis
37	c	11.4	57.0	19	6	AR089229	AR089229 Sequence
38		11.4	57.0	20	6	AR088494	AR088494 Sequence
39	c	11.4	57.0	20	6	AR093007	AR093007 Sequence
40		11.4	57.0	24	6	AR055533	AR055533 Sequence
41		11.4	57.0	24	6	AR082717	AR082717 Sequence
42		11.4	57.0	24	6	AR084859	AR084859 Sequence
43		11.4	57.0	24	6	AR087667	AR087667 Sequence
44		11.4	57.0	24	6	AR094027	AR094027 Sequence
45		11.4	57.0	25	6	AX003410	AX003410 Sequence

ALIGNMENTS

RESULT 1
I34489
LOCUS I34489 33 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 43 from patent US 5597908.
ACCESSION I34489
VERSION I34489.1 GI:1825280
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Taddei-Peters,W.C. and Butler,S.M.
TITLE Immunoreactive peptides of apo(a)
JOURNAL Patent: US 5597908-A 43 28-JAN-1997;
FEATURES Location/Qualifiers
source 1. .33
/organism="unknown"
BASE COUNT 6 a 7 c 10 g 10 t
ORIGIN

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  Query Match           75.0%;  Score 15;  DB 6;  Length 33;
  Best Local Similarity  100.0%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 gtaggttgatgcttc 20
          ||||||||||||||||
Db     13 GTAGGTTGATGCTTC 27


RESULT   2
AX106346/c
LOCUS       AX106346       54 bp    DNA             PAT       30-APR-2001
DEFINITION  Sequence 127 from Patent WO0125272.
ACCESSION   AX106346
VERSION     AX106346.1  GI:13922028
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
  TITLE     Compositions and methods for therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: WO 0125272-A 127 12-APR-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       23 a      17 c       9 g       5 t
ORIGIN


  Query Match           69.0%;  Score 13.8;  DB 6;  Length 54;
  Best Local Similarity  88.2%;  Pred. No. 4.9e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 aagtaggttgatgcttc 20
          |||| | ||||||||||
Db     40 AAGTGGATTGATGCTTC 24


RESULT   3
AX140637/c
LOCUS       AX140637       54 bp    DNA             PAT       31-MAY-2001
DEFINITION  Sequence 127 from Patent WO0134802.
ACCESSION   AX140637
VERSION     AX140637.1  GI:14280751
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
            Skeiky,Y.A. and Wang,A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: WO 0134802-A 127 17-MAY-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT       23 a      17 c       9 g       5 t
ORIGIN


  Query Match           69.0%;  Score 13.8;  DB 6;  Length 54;
  Best Local Similarity  88.2%;  Pred. No. 4.9e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 aagtaggttgatgcttc 20
          |||| | ||||||||||
Db     40 AAGTGGATTGATGCTTC 24


RESULT   4
AX011484
LOCUS       AX011484       59 bp    DNA             PAT       06-SEP-2000
DEFINITION  Sequence 161 from Patent WO9955907.
ACCESSION   AX011484
VERSION     AX011484.1  GI:9998034
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 59)
  AUTHORS   Koetter,P., Entian,K.D. and Diu-Hercend,A.
  TITLE     Method for screening antimycotic substances using essential genes
            from s. Cerevisiae
  JOURNAL   Patent: WO 9955907-A 161 04-NOV-1999;
            KOETTER PETER (DE); ENTIAN KARL DIETER (DE); DIU HERCEND ANITA
            (FR); HOECHST MARION ROUSSEL INC (FR)
FEATURES             Location/Qualifiers
     source          1. .59
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="primer YDR181c-S1"
BASE COUNT       21 a      13 c       13 g      12 t
ORIGIN


  Query Match           68.0%;  Score 13.6;  DB 6;  Length 59;
  Best Local Similarity  80.0%;  Pred. No. 6.4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 tctaagtaggttgatgcttc 20
          |||||||  | ||| |||||
Db     34 TCTAAGTCAGCTGAAGCTTC 53


RESULT   5
AX080760
LOCUS       AX080760       52 bp    DNA             PAT       27-FEB-2001
DEFINITION  Sequence 6 from Patent WO0109327.
ACCESSION   AX080760
VERSION     AX080760.1  GI:13169739
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Ashkenazi,A.J., Baker,K.P., Goddard,A., Godowski,P.J., Gurney,A.L.,
            Kljavin,I.J., Lafleur,M., Mark,M.R., Marsters,S.A., Pitti,R.M.,
            Watanabe,C.K. and Wood,W.I.
  TITLE     Method of preventing the injury or death of retinal cells and
            treating ocular diseases
  JOURNAL   Patent: WO 0109327-A 6 08-FEB-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Hybridization probe."
BASE COUNT       14 a      8 c       13 g      17 t
ORIGIN


  Query Match           64.0%;  Score 12.8;  DB 6;  Length 52;
  Best Local Similarity  87.5%;  Pred. No. 1.8e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy      3 taagtaggttgatgct 18
          ||||| | ||||||||
Db      7 TAAGTGGTTTGATGCT 22


RESULT   6
AR012698
LOCUS       AR012698       34 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 31 from patent US 5763590.
ACCESSION   AR012698
VERSION     AR012698.1  GI:3971016
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Peattie,D.A., Harding,M.W. and Livingston,D.J.
  TITLE     Isolation of an M.sub.r 52,000 FK506 binding protein and molecular
            cloning of a corresponding human cDNA
  JOURNAL   Patent: US 5763590-A 31 09-JUN-1998;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
BASE COUNT        7 a      11 c       4 g      12 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 34;
  Best Local Similarity   78.9%;  Pred. No. 2.3e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 ctaagtaggttgatgcttc 20
          |||| || | | |||||||
Db      6 CTAATTAAGCTTATGCTTC 24


RESULT   7
AR023824/c
LOCUS       AR023824       56 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 31 from patent US 5795746.
ACCESSION   AR023824
VERSION     AR023824.1  GI:3977118
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Kjeldsen,T.B.oslashed.rglum and Vad,K.
  TITLE     Synthetic leader peptide sequences
  JOURNAL   Patent: US 5795746-A 31 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .56
                     /organism="unknown"
BASE COUNT       21 a      12 c      10 g      13 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 56;
  Best Local Similarity   78.9%;  Pred. No. 2.4e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 tctaagtaggttgatgctt 19
          ||| | | |||||| ||||
Db     26 TCTCACTTGGTTGAAGCTT 8


RESULT   8
I46850/c
LOCUS       I46850         56 bp    DNA             PAT       07-OCT-1997
DEFINITION  Sequence 31 from patent US 5639642.
ACCESSION   I46850
VERSION     I46850.1  GI:2470815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Kjeldsen,T.B.oslashed.rglum and Vad,K.
  TITLE     Synthetic leader peptide sequences
  JOURNAL   Patent: US 5639642-A 31 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .56
                     /organism="unknown"
BASE COUNT       21 a      12 c      10 g      13 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 56;
  Best Local Similarity   78.9%;  Pred. No. 2.4e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 tctaagtaggttgatgctt 19
          ||| | | |||||| ||||
Db     26 TCTCACTTGGTTGAAGCTT 8


RESULT   9
DROPEIS8/c
LOCUS       DROPEIS8       58 bp    DNA             INV       03-FEB-1999
DEFINITION  D.melanogaster DNA, P element insertion site.
ACCESSION   D12606
VERSION     D12606.1  GI:393304
KEYWORDS    P element insertion site; transformation.
SOURCE      Drosophila melanogaster (isolate:#150508) adult whole body DNA.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 58)
  AUTHORS   Togashi,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-1992) to the DDBJ/EMBL/GenBank databases. Shin
            Togashi, Mitsubishi Kasei Institute of Life Sciences, Laboratory of
            Cell Biology; 11 Minamiooya, Machida-shi, Tokyo 194, Japan
            (Tel:0427-24-6249, Fax:0427-29-1252)
REFERENCE   2  (bases 1 to 58)
  AUTHORS   Togashi,S., Ueda,R., Takahisa,M., Mikuni,M., Kondo,K. and Miyake,T.
  TITLE     Insertional mutagenesis in Drosophila. II. P element mediated
            transformation of Drosophila yakuba
  JOURNAL   Jpn. J. Genet. 67 (4), 291-297 (1992)
  MEDLINE   93199819
COMMENT     Submitted (10-JUL-1992) to DDBJ by:
            Shin Togashi
            Lab. of Cell Biology
            Mitsubishi Kasei Institute of Life Sciences
            11 Minamiooya, Machida-shi
            Tokyo 194
            Japan
            Phone:  0427-24-6249
            Fax:    0427-29-1252.
FEATURES             Location/Qualifiers
     source          1. .58
                     /organism="Drosophila melanogaster"
                     /isolate="#150508"
                     /db_xref="taxon:7227"
                     /dev_stage="adult"
                     /tissue_type="whole body"
     misc_feature    26. .33
                     /note="P element insertion site"
                     /evidence=experimental
BASE COUNT       16 a      14 c      15 g      13 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 3;  Length 58;
  Best Local Similarity   78.9%;  Pred. No. 2.4e+04;
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  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 ctaagtaggttgatgcttc 20
          || ||| || || ||||||
Db     40 CTCAGTGGGCTGCTGCTTC 22


RESULT  10
E04190
LOCUS       E04190         29 bp    DNA             PAT       29-SEP-1997
DEFINITION  linker DNA.
ACCESSION   E04190
VERSION     E04190.1  GI:2172400
KEYWORDS    JP 1993001099-A/18.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Morita,K., Hasegawa,M., Yokoo,Y., Sato,M., Sekine,S., Sugimoto,S.,
            Koda,H., Mori,H. and Arima,T. .
  TITLE     FUSED ANTIGENIC POLYPEPTIDE
  JOURNAL   Patent: JP 1993001099-A 18 08-JAN-1993;
            KYOWA HAKKO KOGYO CO LTD
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1993001099-A/18
            PD   08-JAN-1993
            PF   25-JUN-1991 JP 1991153031
            PI   MORITA KAZUKI, HASEGAWA MAMORU, YOKOO YOSHIHARU, SATO
            MORIYUKI, PI   SEKINE SUSUMU, SUGIMOTO SEIJI, KODA HAJIME, MORI
            HIDEJI, PI   ARIMA TERUMASA
            PC   C07K7/10,C07K13/00,C12N1/21,C12N15/62,C12N15/70,C12P21/02, PC
             C12Q1/68,
            PC   G01N33/569,G01N33/576//A61K39/00,C12N15/51,(C12N1/21,
            C12R1:19), PC   (C12P21/02,
            PC   C12R1:19),C07K99:00;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="synthetic construct"
                      /db_xref="taxon:32630"
BASE COUNT       12 a       3 c       6 g       8 t
ORIGIN


  Query Match             61.0%;  Score 12.2;  DB 6;  Length 29;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 tctaagtaggttgatgc 17
          |||||||| ||  ||||
Db     12 TCTAAGTAAGTAAATGC 28


RESULT  11
E04195
LOCUS       E04195         29 bp    DNA             PAT       29-SEP-1997
DEFINITION  linker DNA.
ACCESSION   E04195
VERSION     E04195.1  GI:2172405
KEYWORDS    JP 1993001099-A/23.
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Morita,K., Hasegawa,M., Yokoo,Y., Sato,M., Sekine,S., Sugimoto,S.,
            Koda,H., Mori,H. and Arima,T. .
  TITLE     FUSED ANTIGENIC POLYPEPTIDE
  JOURNAL   Patent: JP 1993001099-A 23 08-JAN-1993;
            KYOWA HAKKO KOGYO CO LTD
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1993001099-A/23
            PD   08-JAN-1993
            PF   25-JUN-1991 JP 1991153031
            PI   MORITA KAZUKI, HASEGAWA MAMORU, YOKOO YOSHIHARU, SATO
            MORIYUKI, PI   SEKINE SUSUMU, SUGIMOTO SEIJI, KODA HAJIME, MORI
            HIDEJI, PI   ARIMA TERUMASA
            PC   C07K7/10,C07K13/00,C12N1/21,C12N15/62,C12N15/70,C12P21/02, PC
             C12Q1/68,
            PC   G01N33/569,G01N33/576//A61K39/00,C12N15/51,(C12N1/21,
            C12R1:19), PC   (C12P21/02,
            PC   C12R1:19),C07K99:00;
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="synthetic construct"
                      /db_xref="taxon:32630"
BASE COUNT       12 a       3 c       6 g       8 t
ORIGIN


  Query Match             61.0%;  Score 12.2;  DB 6;  Length 29;
  Best Local Similarity   82.4%;  Pred. No. 3.9e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 tctaagtaggttgatgc 17
          |||||||| ||  ||||
Db     12 TCTAAGTAAGTAAATGC 28


RESULT  12
AX167992
LOCUS       AX167992       35 bp    DNA             PAT       03-JUL-2001
DEFINITION  Sequence 176 from Patent WO0142307.
ACCESSION   AX167992
VERSION     AX167992.1  GI:14597312
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Saito,K., Ohe,N. and Satoh,H.
  TITLE     Mutant er_g(a) and test systems for transactivation
  JOURNAL   Patent: WO 0142307-A 176 14-JUN-2001;
            Sumitomo Chemical Company, Limited (JP)
FEATURES              Location/Qualifiers
     source           1. .35
                      /organism="synthetic construct"
                      /db_xref="taxon:32630"
                      /note="Description of Artificial Sequence :Designed
                      oligonucleotide primer for PCR"
BASE COUNT       10 a       3 c      17 g       5 t
ORIGIN


  Query Match             61.0%;  Score 12.2;  DB 6;  Length 35;
  Best Local Similarity   82.4%;  Pred. No. 4e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      4 aagtaggttgatgcttc 20
          |||||||| || | |||
Db     16 AAGTAGGTGGAAGATTC 32


RESULT  13
A92655
LOCUS       A92655         24 bp    DNA             PAT       22-JAN-2000
DEFINITION  Sequence 3 from Patent WO9806831.
ACCESSION   A92655
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VERSION     A92655.1  GI:6741295
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   La,C.U. and Willmitzer,L.
  TITLE     TRANSGENIC PLANT CELLS AND PLANTS WITH MODIFIED ACETYL-COA
            FORMATION
  JOURNAL   Patent: WO 9806831-A 3 19-FEB-1998;
            MAX PLANCK GESELLSCHAFT (DE); WILLMITZER LOTHAR (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        5 a      5 c      4 g     10 t
ORIGIN


  Query Match           60.0%;  Score 12;  DB 6;  Length 24;
  Best Local Similarity   75.0%;  Pred. No. 5.1e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 tctaagtaggttgatgcttc 20
          | || ||| |||  ||||||
Db      2 TATACGTAAGTTTCTGCTTC 21


RESULT  14
E13871/c
LOCUS       E13871          28 bp    DNA             PAT       24-JUN-1998
DEFINITION  PCR primer for gaining Treponema hybrid antigen.
ACCESSION   E13871
VERSION     E13871.1  GI:3252638
KEYWORDS    JP 1997235298-A/27.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Ise,N., Hori,T., Fujimura,K., Tanimoto,T. and Okada,M. .
  TITLE     PALLIDUM TREPONEMA FUSED ANTIGEN AND ASSAY OF ANTI-PALLIDUM
            TREPONEMA ANTIBODY USING THE SAME
  JOURNAL   Patent: JP 1997235298-A 27 09-SEP-1997;
            FUJIREBIO INC
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997235298-A/27
            PD   09-SEP-1997
            PF   25-DEC-1996 JP 1996355804
            PR   25-DEC-1995 JP 95P   350072
            PI   ISE NOBUYUKI, HORI TAKEYA, FUJIMURA KATSUYA, TANIMOTO TETSUJI,
            PI   OKADA MASAHISA
            PC   C07K14/20,C12N15/09,G01N33/531,G01N33/571//C12P21/02,
            C12P21/08, PC   (C12P21/02,
            PC   C12R1:19);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .28
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        7 a      8 c      6 g      7 t
ORIGIN


  Query Match           60.0%;  Score 12;  DB 6;  Length 28;
  Best Local Similarity   75.0%;  Pred. No. 5.1e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 tctaagtaggttgatgcttc 20
          | | || |||| || |||||
Db     23 TATTAGCAGGTAGAAGCTTC 4


RESULT  15
AR134189/c
LOCUS       AR134189        54 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 2614 from patent US 6194150.
ACCESSION   AR134189
VERSION     AR134189.1  GI:14123094
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
  TITLE     Nucleic acid based inhibition of CD40
  JOURNAL   Patent: US 6194150-A 2614 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="unknown"
BASE COUNT       20 a     11 c     12 g     11 t
ORIGIN


  Query Match           60.0%;  Score 12;  DB 6;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      9 ggttgatgcttc 20
          ||||||||||||
Db     21 GGTTGATGCTTC 10


Search completed: March 13, 2002, 10:38:52
Job time: 4149 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 10:55:14 ; Search time 968.42 Seconds
(without alignments)
17.706 Million cell updates/sec

Title: US-09-923-515-34
Perfect score: 20
Sequence: 1 ctggcggtgaccatgtagtc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	20	100.0	39	16	AAQ91613	Human apolipoprote
	2	14.2	71.0	42	21	AAC89310	Primer REPSPS5. S
c	3	14.2	71.0	50	21	AAC87174	Maize Adh1 intron
c	4	14.2	71.0	50	21	AAC88384	Primer Adh3. Synt
c	5	14.2	71.0	50	21	AAC89300	Primer Adh3. Synt
c	6	14	70.0	17	21	AAF02295	Hammerhead ribozym
	7	13.6	68.0	24	21	AAZ52312	Backward 5' RACE-P
c	8	13.6	68.0	40	20	AAZ27005	Human chromosome 1
c	9	13.4	67.0	20	19	AAV05043	PCR primer of the
	10	13.4	67.0	47	21	AAZ67280	Human map-related
c	11	13.2	66.0	28	21	AAC66048	E.coli ygbP primer
	12	12.8	64.0	21	22	AAC67031	ALV stva-mIgG prot
	13	12.8	64.0	24	21	AAA66374	Dog genomic marker
c	14	12.8	64.0	27	22	AAF31123	Mutagenic primer #
c	15	12.8	64.0	29	19	AAV40536	Homo sapiens CZ268
c	16	12.6	63.0	31	17	AAT45762	Human stem cell fa
c	17	12.6	63.0	42	21	AAA07016	Raf-1 mutagenic PC
	18	12.6	63.0	47	21	AAZ67033	Human map-related
c	19	12.6	63.0	48	20	AAV63790	Primer used for fi
	20	12.4	62.0	30	21	AAZ35208	Corn globulin-1 ge
	21	12.4	62.0	39	21	AAC87176	Maize Adh1 intron
c	22	12.4	62.0	39	21	AAC87177	Maize Adh1 intron
	23	12.4	62.0	39	21	AAC88386	Primer Oskozak. S
c	24	12.4	62.0	39	21	AAC88387	Primer Oskozakrev.
	25	12.4	62.0	39	21	AAC89302	Primer Oskozak. S
c	26	12.4	62.0	39	21	AAC89303	Primer Oskozakrev.
	27	12.2	61.0	18	21	AAZ57721	Human G-alpha-12 a
	28	12.2	61.0	21	21	AAZ74889	Human biallelic ma
c	29	12.2	61.0	24	14	AAQ43318	Sequence of sense
	30	12.2	61.0	25	22	AAH23624	RNA binding protei
	31	12.2	61.0	25	22	AAS00233	Afx transcription
c	32	12.2	61.0	28	17	AAX90411	S. lividans xylana
c	33	12.2	61.0	28	18	AAT64940	Sense primer S. li
c	34	12.2	61.0	30	22	AAF86279	PCR primer for pre
c	35	12.2	61.0	35	15	AAQ72996	Cowpox virus fragm
	36	12.2	61.0	38	21	AAA08968	Primer 2 for human
c	37	12.2	61.0	42	22	AAC88699	Mannanase sequenci
c	38	12.2	61.0	45	21	AAA07694	HERG gene intragen
	39	12.2	61.0	46	22	AAF86303	PCR primer for tra
	40	12.2	61.0	47	22	AAF86287	PCR primer for tra
	41	12	60.0	23	14	AAQ38983	Sequence of revers
c	42	12	60.0	31	16	AAQ94500	Human/murine chime
c	43	12	60.0	31	16	AAQ75904	Primer FTY-1 to mu
c	44	12	60.0	31	17	AAT38614	Chimaeric MAb ONS-
c	45	12	60.0	31	19	AAV39387	Humanised anti-HM1

ALIGNMENTS

RESULT 1
AAQ91613/c
ID AAQ91613 standard; DNA; 39 BP.
XX
AC AAQ91613;
XX
DT 05-FEB-1996 (first entry)
XX
DE Human apolipoprotein (a) (apo(a)) primer/probe.
XX
KW Human; old world monkey; apolipoprotein (a); apo(a); primer; probe;
KW antigenic peptide; immunoassay; detection; quantification; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..39
FT /*tag= a
XX
PN EP659765-A2.
XX
PD 28-JUN-1995.
XX
PF 16-DEC-1994; 94EP-0203653.
XX
PR 27-JUN-1994; 94US-0266407.
PR 21-DEC-1993; 93US-0172461.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Butler SM, Taddei-peters WC;
XX
DR WPI; 1995-226203/30.
DR P-PSDB; AAR77320.

```
XX
PT   New immuno:reactive peptide(s) of apo:lipoprotein - used for prodn.
PT   of antibodies and development of immunoassays, for the detection and
PT   quantification of apo(a)
XX
PS   Claim 18; Page 15; 44pp; English.
XX
CC   AAQ91613 encodes AAR77320 a human/old world monkey apolipoprotein (a)
CC   (apo(a)) antigenic peptide. The peptide can be used to raise anti-
CC   apo(a) antibodies, for use in immunoassays for the detection of
CC   apo(a). The DNA sequence can be used as a primer and/or probe for
CC   the detection, and quantification of apo(a) DNA.
XX
SQ   Sequence 39 BP; 11 A; 12 C; 8 G; 8 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 16;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 0.65;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctggcggtgaccatgtagtc 20
           ||||||||||||||||||||
Db      23 CTGGCGGTGACCATGTAGTC 4


RESULT   2
AAC89310
ID   AAC89310 standard; DNA; 42 BP.
XX
AC   AAC89310;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Primer REPSPS5.
XX
KW   5-enolpyruvylshikimate phosphate synthase; EPSPS;
KW   herbicide resistance; glyphosate; ss.
XX
OS   Synthetic.
XX
PN   WO200066747-A1.
XX
PD   09-NOV-2000.
XX
PF   20-APR-2000; 2000WO-GB01572.
XX
PR   29-APR-1999;   99GB-0009967.
PR   29-APR-1999;   99GB-0009969.
PR   29-APR-1999;   99GB-0009972.
PR   29-APR-1999;   99GB-0009981.
PR   29-APR-1999;   99GB-0017835.
PR   29-JUL-1999;   99GB-0017836.
PR   29-JUL-1999;   99GB-0017843.
PR   21-DEC-1999;   99GB-0030202.
PR   21-DEC-1999;   99GB-0030210.
PR   21-DEC-1999;   99GB-0030212.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Hawkes TR,  Warner SAJ,  Andrews CJ,  Bachoo S,  Pickerill AP;
XX
DR   WPI; 2000-679764/66.
XX
PT   Isolated polynucleotide encoding a 5-enolpyruvylshikimate phosphate
PT   synthase from rice is used for producing transgenic plants with
PT   enhanced resistance to glyphosate herbicide -
XX
PS   Example 8; Page 18; 98pp; English.
XX
CC   The present invention relates to an Oryza sp. 5-enolpyruvylshikimate
CC   phosphate synthase (EPSPS) gene. Vectors containing the gene may be
CC   used to produce plant tissues and fertile whole plants which are
CC   substantially tolerant or substantially resistant to glyphosate
CC   herbicide and to produce a herbicidal target which is used for high
CC   throughput in vitro screening of potential herbicides.
XX
SQ   Sequence 42 BP; 4 A; 13 C; 14 G; 11 T; 0 other;


  Query Match             71.0%;  Score 14.2;  DB 21;  Length 42;
  Best Local Similarity   84.2%;  Pred. No. 5e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 tggcggtgaccatgtagtc 20
           ||||||  |||||||  |||
Db      23 tggcggcgaccatggcgtc 41


RESULT   3
AAC87174/c
ID   AAC87174 standard; DNA; 50 BP.
XX
AC   AAC87174;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Maize Adh1 intron 1 PCR primer, SEQ ID NO:29.
XX
KW   Rice EPSPS; 5-enolpyruvylshikimate phosphate synthase;
KW   glyphosate resistance; herbicide resistance; transgenic plant;
KW   expression construct; maize Adh1 intron 1; PCR primer; ss.
XX
OS   Zea mays.
XX
PN   WO200066748-A1.
XX
PD   09-NOV-2000.
XX
PF   20-APR-2000; 2000WO-GB01573.
XX
PR   29-APR-1999;   99GB-0009968.
PR   29-APR-1999;   99GB-0017834.
PR   29-APR-1999;   99GB-0030213.
PR   29-JUL-1999;   99GB-0017839.
PR   29-JUL-1999;   99GB-0017840.
PR   29-JUL-1999;   99GB-0017846.
PR   29-JUL-1999;   99GB-0017847.
PR   21-DEC-1999;   99GB-0030200.
PR   21-DEC-1999;   99GB-0030204.
PR   21-DEC-1999;   99GB-0030207.
PR   21-DEC-1999;   99GB-0030209.
XX
PA   (ZENE ) ZENECA LTD.
XX
PI   Hawkes TR,  Warner SAJ,  Andrews CJ,  Bachoo S,  Pickerill AP;
XX
DR   WPI; 2000-687544/67.
XX
PT   Novel polynucleotide encoding 5-enolpyruvylshikimate phosphate
PT   synthase, used to produce transgenic plants e.g. banana, wheat, maize
PT   or rice, having resistance or tolerance to glyphosate herbicide -
XX
PS   Example 6; Page 18; 87pp; English.
XX
CC   The invention relates to rice 5-enolpyruvylshikimate phosphate synthase
CC   (EPSPS) genomic DNA (AAC87188). The invention also relates to an
CC   expression cassette comprising, in the 5'-3' direction, one or more
CC   transcriptional enhancer elements selected from AAC87190-C87196), the
CC   rice EPSPS promoter, genomic DNA encoding a rice EPSPS chloroplast
CC   transit peptide, genomic DNA encoding a EPSPS protein modified such that
CC   it is resistant to glyphosate (AAC87189), and a transcriptional
CC   terminator. The glyphosate resistant EPSPS contains a region (AAB29793)
CC   containing two amino acid substitutions relative to the corresponding
CC   wild-type region (AAB29792). The invention also encompasses plant genomic
CC   EPSPS sequences identified via screening with a rice EPSPS intronic
CC   sequence; vectors and host plant cells comprising a nucleic acid sequence
```

CC of the invention; transgenic plants (and tissues and seeds thereof)
CC comprising a nucleic acid sequence of the invention, optionally further
CC transformed with a DNA encoding an insect, fungal, viral, bacterial,
CC nematode, stress or herbicide resistance protein; and methods of
CC producing the transgenic plants of the invention. The nucleic acids and
CC constructs of the invention are used to produce a wide variety of
CC morphologically normal, glyphosate resistant plants. The glyphosate
CC resistant plants produced are particularly maize, soybean, cotton,
CC sugarbeet and canola, but also other field crops, fruits and vegetables,
CC turf and forage grasses and nut-producing plants. The plants are
CC optionally resistant to insects, fungi, viruses, bacteria, nematodes,
CC stress, desiccation and/or other herbicides. They can be used in the
CC production of a herbicidal target for the high throughput in vitro
CC screening of potential herbicides. The present sequence represents a PCR
CC primer used in an exemplification of the invention.
XX
SQ Sequence 50 BP; 11 A; 18 C; 15 G; 6 T; 0 other;

Query Match 71.0%; Score 14.2; DB 21; Length 50;
Best Local Similarity 84.2%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tggcggtgaccatgtagtc 20
|||||| ||||||| |||
Db 19 TGGCGGCGACCATGGCGTC 1

RESULT 4
AAC88384/c
ID AAC88384 standard; DNA; 50 BP.
XX
AC AAC88384;
XX
DT 02-MAR-2001 (first entry)
XX
DE Primer Adh3.
XX
KW Glyphosate; 5-enolpyruvylshikimate phosphate synthase; EPSPS;
KW herbicide resistance; ss.
XX
OS Synthetic.
XX
PN WO200066746-A1.
XX
PD 09-NOV-2000.
XX
PF 20-APR-2000; 2000WO-GB01559.
XX
PR 29-APR-1999; 99GB-0009971.
PR 29-APR-1999; 99GB-0009972.
PR 29-JUL-1999; 99GB-0017837.
PR 29-JUL-1999; 99GB-0017842.
PR 21-DEC-1999; 99GB-0030190.
PR 21-DEC-1999; 99GB-0030206.
PR 21-DEC-1999; 99GB-0030214.
PR 21-DEC-1999; 99GB-0030216.
XX
PA (ZENE) ZENECA LTD.
XX
PI Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;
XX
DR WPI; 2000-679763/66.
XX
PT Novel polynucleotide encoding the rice 5-enolpyruvylshikimate phosphate
PT synthase, used to produce glyphosate tolerant or resistant plants -
XX
PS Example 6; Page 16; 85pp; English.
XX
CC The present invention relates to a glyphosate resistant rice
CC 5-enolpyruvylshikimate phosphate synthase (EPSPS) gene. This gene can
CC be used to produce plant tissue and/or morphologically normal fertile
CC whole plants which are tolerant or resistant to glyphosate herbicide,
CC and in the production of a herbicidal target for the high throughput
CC in vitro screening of potential herbicides.
XX
SQ Sequence 50 BP; 11 A; 18 C; 15 G; 6 T; 0 other;

Query Match 71.0%; Score 14.2; DB 21; Length 50;
Best Local Similarity 84.2%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 tggcggtgaccatgtagtc 20
|||||| ||||||| |||
Db 19 TGGCGGCGACCATGGCGTC 1

RESULT 5
AAC89300/c
ID AAC89300 standard; DNA; 50 BP.
XX
AC AAC89300;
XX
DT 07-MAR-2001 (first entry)
XX
DE Primer Adh3.
XX
KW 5-enolpyruvylshikimate phosphate synthase; EPSPS;
KW herbicide resistance; glyphosate; ss.
XX
OS Synthetic.
XX
PN WO200066747-A1.
XX
PD 09-NOV-2000.
XX
PF 20-APR-2000; 2000WO-GB01572.
XX
PR 29-APR-1999; 99GB-0009967.
PR 29-APR-1999; 99GB-0009969.
PR 29-APR-1999; 99GB-0009972.
PR 29-APR-1999; 99GB-0009981.
PR 29-APR-1999; 99GB-0017835.
PR 29-JUL-1999; 99GB-0017836.
PR 29-JUL-1999; 99GB-0017843.
PR 21-DEC-1999; 99GB-0030202.
PR 21-DEC-1999; 99GB-0030210.
PR 21-DEC-1999; 99GB-0030212.
XX
PA (ZENE) ZENECA LTD.
XX
PI Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;
XX
DR WPI; 2000-679764/66.
XX
PT Isolated polynucleotide encoding a 5-enolpyruvylshikimate phosphate
PT synthase from rice is used for producing transgenic plants with
PT enhanced resistance to glyphosate herbicide -
XX
PS Example 6; Page 16; 98pp; English.
XX
CC The present invention relates to an Oryza sp. 5-enolpyruvylshikimate
CC phosphate synthase (EPSPS) gene. Vectors containing the gene may be
CC used to produce plant tissues and fertile whole plants which are
CC substantially tolerant or substantially resistant to glyphosate
CC herbicide and to produce a herbicidal target which is used for high
CC throughput in vitro screening of potential herbicides.
XX
SQ Sequence 50 BP; 11 A; 18 C; 15 G; 6 T; 0 other;

Query Match 71.0%; Score 14.2; DB 21; Length 50;
Best Local Similarity 84.2%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      2 tggcggtgaccatgtagtc 20
          |||||| |||||||  |||
Db     19 TGGCGGCGACCATGGCGTC 1


RESULT   6
AAF02295/c
ID   AAF02295 standard; DNA; 17 BP.
XX
AC   AAF02295;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Hammerhead ribozyme substrate #590.
XX
KW   Ribozyme; erythropoietin; granulocyte colony stimulating factor;
KW   interferon alpha; ss.
XX
OS   Homo sapiens.
XX
PN   WO200061729-A2.
XX
PD   19-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US09721.
XX
PR   12-APR-1999;   99US-0129390.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Blatt L,  Zwick M,  Pavco P,  McSwiggen J;
XX
DR   WPI; 2000-647423/62.
XX
PT   Enzymatic and antisense nucleic acid inhibition of repressor genes,
PT   useful for producing e.g. granulocyte colony stimulating factor
PT   protein, interferon alpha and erythropoietin -
XX
PS   Claim 37; Page 69; 164pp; English.
XX
CC   The present invention relates to enzymatic and antisense nucleic acid
CC   molecules that act as inhibitors of the expression of repressor genes
CC   encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
CC   transcription factor gene, IRF-2 and/or the CAATT Displacement
CC   Protein (CDP). Inhibition of the repressors removes prevents
CC   inhibition (and consequently increases expression of) genes involved in
CC   the production of erythropoietin, granulocyte colony stimulating factor
CC   protein and interferon alpha.
XX
SQ   Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 other;


  Query Match             70.0%;  Score 14;  DB 21;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 tggcggtgaccatg 15
          ||||||||||||||
Db     16 TGGCGGTGACCATG 3


RESULT   7
AAZ52312
ID   AAZ52312 standard; DNA; 24 BP.
XX
AC   AAZ52312;
XX
DT   18-JUL-2000  (first entry)
XX
DE   Backward 5' RACE-PCR primer to obtain rat pancreatic T-type Ca2+ channel.
XX
KW   Rat; pancreatic T-type calcium channel alpha1 subunit; insulin;
KW   pancreatic beta cell; alpha1G; low voltage activated Ca2+ channel family;
KW   antidiabetic; calcium influx; L type calcium channel; PCR primer;
KW   type II diabetes; NIDDM; non-insulin dependent diabetes mellitus;
KW   RACE; rapid amplification of cDNA ends; ss.
XX
OS   Rattus sp.
XX
PN   WO200015845-A1.
XX
PD   23-MAR-2000.
XX
PF   26-AUG-1999;   99WO-US19675.
XX
PR   26-AUG-1998;   98US-0098004.
PR   27-JAN-1999;   99US-0117399.
XX
PA   (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
XX
PI   Li M;
XX
DR   WPI; 2000-271475/23.
XX
PT   Novel nucleic acids encoding pancreatic T-type calcium channels used
PT   for regulation of T-type calcium channels and treatment of type II
PT   diabetes -
XX
PS   Disclosure; Page 47; 124pp; English.
XX
CC   The present sequence is the backward 5' RACE-PCR primer, used along with
CC   an adapter as forward primer, to obtain the entire gene of rat T-type
CC   calcium channel alpha1 subunit from insulin secreting beta cell line,
CC   INS-1. The pancreatic T-type calcium channel alpha1 subunit has 96.3 %
CC   identity to the neuronal T-type calcium channel alpha1 subunit (alpha1G).
CC   The T-type Ca2+ channel from INS-1 (alpha1G-INS) and neuronal alpha1G are
CC   alternative splice isoforms of the same gene. The INS-1 isoform is also
CC   expressed in brain, neonatal heart and kidney, besides pancreatic beta
CC   cells. T-type Ca2+ channel belongs to the family of low voltage activated
CC   Ca2+ channels. It is used for treating diseases associated with abnormal
CC   expression or function of T-type calcium channels. They are especially
CC   used for treating type II diabetes. Modulators of pancreatic T-type Ca2+
CC   channel e.g. antisense oligonucleotides, ribozymes and inhibitors are
CC   used in methods for modifying insulin secretion by pancreatic beta cells,
CC   basal calcium levels, potential L type calcium channel activity,
CC   pancreatic cell death, pancreatic beta cell proliferation and calcium
CC   influx through L type calcium channels in cells.
XX
SQ   Sequence 24 BP; 5 A; 8 C; 8 G; 3 T; 0 other;


  Query Match             68.0%;  Score 13.6;  DB 21;  Length 24;
  Best Local Similarity   80.0%;  Pred. No. 9.4e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ctggcggtgaccatgtagtc 20
          ||| ||| ||||||| || |
Db      4 ctgtcggagaccatggagac 23


RESULT   8
AAZ27005/c
ID   AAZ27005 standard; DNA; 40 BP.
XX
AC   AAZ27005;
XX
DT   18-NOV-1999  (first entry)
XX
DE   Human chromosome 11 linked CHD1 gene mutation screening PCR primer #143.
XX
KW   Human; coronary heart disease susceptibility gene; CHD1; mutation;
KW   chromosome 11; diagnosis; screening; PCR primer; metabolic disorder;
KW   detection; hypoalphalipoproteinaemia; familial combined hyperlipidaemia;
KW   insulin resistant syndrome X; multiple metabolic disorder; obesity;
KW   diabetes; dyslipidaemic hypertension; ss.
XX
```

```
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9945112-A2.
XX
PD   10-SEP-1999.
XX
PF   04-MAR-1999;   99WO-US04682.
XX
PR   04-MAR-1998;   98US-0034941.
PR   06-APR-1998;   98US-0080934.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Ballinger DG,  Ding W,  Wagner S,  Hess MA;
XX
DR   WPI; 1999-540844/45.
XX
PT   New isolated coronary heart disease susceptibility gene, used to
PT   develop products for diagnosis and treatment of coronary heart disease
PT   and metabolic disorders  -
XX
PS   Example 6; Page 104; 297pp; English.
XX
CC   The present invention describes the human chromosome 11-linked coronary
CC   heart disease susceptibility gene (CHD1). Mutations in the CHD1 locus
CC   in the germline are indicative of a predisposition to coronary heart
CC   disease or to metabolic disorders related to lipid metabolism.
CC   Products from the present invention can be used in the diagnosis
CC   of predisposition to coronary heart disease and to metabolic disorders,
CC   including hypoalphalipoproteinaemia, familial combined hyperlipidaemia,
CC   insulin resistant syndrome X or multiple metabolic disorder, obesity,
CC   diabetes and dyslipidaemic hypertension. CHD1 proteins can be used for
CC   treating coronary heart disease and metabolic disorders. The products
CC   can also be used for detection and drug screening. AAZ26832 to AAZ26841
CC   and AAZ27027 to AAZ27029 represent human CHD1 nucleotide sequences.
CC   AAY29917 to AAY29926 represent human CHD1 proteins and protein sequences
CC   used in the exemplification of the present invention. AAZ26842 to
CC   AAZ26862 represent primers used in the identification of human CHD1;
CC   AAZ26863 to AAZ27014 represent PCR primers used in the screening of
CC   mutations in human CHD1; AAZ27015 to AAZ27026 represent oligonucleotides
CC   used in the exemplification of the present invention.
XX
SQ   Sequence 40 BP; 8 A; 13 C; 10 G; 9 T; 0 other;


  Query Match             68.0%;  Score 13.6;  DB 20;  Length 40;
  Best Local Similarity   80.0%;  Pred. No. 9.9e+02;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 ctggcggtgaccatgtagtc 20
           ||||| |||| ||||  |||
Db      34 CTGGCCGTGAACATGGCGTC 15


RESULT   9
AAV05043/c
ID   AAV05043 standard; cDNA to mRNA; 20 BP.
XX
AC   AAV05043;
XX
DT   12-MAY-1998  (first entry)
XX
DE   PCR primer of the specification.
XX
KW   Vasopressin V1b receptor; detection; drug; PCR primer; amplify; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   JP07327676-A.
XX
PD   19-DEC-1995.
XX
PF   06-JUN-1994;   94JP-0124028.
XX
PR   06-JUN-1994;   94JP-0124028.
XX
PA   (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
DR   WPI; 1998-171834/16.
XX
PT   Vasopressin V1b receptor polypeptide - useful for detecting and
PT   evaluating drugs reacting with vasopressin V1b receptor
XX
PS   Disclosure; Page 8; 13pp; Japanese.
XX
CC   PCR primers AAV05042-43 are primers of the specification. The
CC   specification describes a novel human vasopressin V1b receptor
CC   polypeptide (and DNA encoding it). The products are useful for
CC   the detection and evaluation of drugs reacting with vasopressin
CC   V1b receptor.
XX
SQ   Sequence 20 BP; 5 A; 5 C; 7 G; 3 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 19;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 1.2e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 ctggcggtgaccatg 15
           ||| ||||||||||
Db      19 CTGCCGGTGACCATG 5


RESULT  10
AAZ67280
ID   AAZ67280 standard; DNA; 47 BP.
XX
AC   AAZ67280;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:1627.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,G)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome  -
XX
PS   Claim 1; Page 577; 2745pp; English.
```

XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 17 A; 9 C; 10 G; 11 T; 0 other;

Query Match 67.0%; Score 13.4; DB 21; Length 47;
Best Local Similarity 93.3%; Pred. No. 1.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 ggtgaccatgtagtc 20
|||||||||| ||||
Db 4 ggtgaccatgaagtc 18

RESULT 11
AAC66048/c
ID AAC66048 standard; DNA; 28 BP.
XX
AC AAC66048;
XX
DT 22-FEB-2001 (first entry)
XX
DE E.coli ygbP primer YGBP1A.
XX
KW YJEE; KDTB; YQGF; YGGF; YHBC; YGBP; YGBB; YCHB; antibacterial;
KW treatment; infection; primer; ss.
XX
OS Escherichia coli.
XX
PN DE19916176-A1.
XX
PD 12-OCT-2000.
XX
PF 10-APR-1999; 99DE-1016176.
XX
PR 10-APR-1999; 99DE-1016176.
XX
PA (FARB) BAYER AG.
XX
PI Broetz H, Ehlert K, Freiberg C, Spaltmann F, Wieland B;
PI Labischinski H;
XX
DR WPI; 2000-639611/62.
XX
PT Essential genes from bacteria, useful in screening for antimicrobial
PT agents, and related proteins, transformants and antisense sequences -
XX
PS Example 2; Page 25; 28pp; German.
XX
CC This invention describes novel Escherichia coli genes (I) encoding
CC proteins (II) designated YQGF, YHBC, YGGJ, YGBP, YCHB, YGBB, YJEE and
CC KDTB, and genes (Ia) that encode orthologous gene products (IIa) in
CC other microorganisms and which have antibacterial activity. Recombinant
CC microorganisms in which expression of (I) or (Ia) can be regulated are
CC used to identify compounds that bind to the gene products, particularly
CC in affinity selection assays. (II) and (IIa) are used to identify, or
CC prepare, antibodies and other proteins that bind to the gene products.
CC Substances that bind to (II) or (IIa) are potentially useful as
CC antibacterials for treating a wide range of infections in humans and
CC animals. Sequences antisense to (I) and (Ia) can also be used as
CC antibacterials. The specified genes are widely distributed in bacteria
CC but have no close homologs in eukaryotic cells.
XX
SQ Sequence 28 BP; 4 A; 11 C; 8 G; 5 T; 0 other;

Query Match 66.0%; Score 13.2; DB 21; Length 28;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ctggcggtgaccatgtag 18
| ||| |||||||||| |
Db 27 CAGGCAGTGACCATGTGG 10

RESULT 12
AAC67031
ID AAC67031 standard; DNA; 21 BP.
XX
AC AAC67031;
XX
DT 27-MAR-2001 (first entry)
XX
DE ALV stva-mIgG protein PCR primer SEQ ID NO: 31.
XX
KW Xenotransplantation; infectious agent; vaccine; PCR primer; ss.
XX
OS Avian leukosis virus.
XX
PN WO200071726-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-US14296.
XX
PR 24-MAY-1999; 99US-0135631.
XX
PA (MAYO-) MAYO MEDICAL VENTURES.
XX
PI Federspiel MJ;
XX
DR WPI; 2001-032041/04.
XX
PT Inhibiting or preventing infectious agent transmission in mammalian
PT transplant recipients, by introducing recombinant DNA comprising DNA
PT encoding extracellular proteins of the agent into donor cells, such as
PT swine cells -
XX
PS Example 5; Page 59; 144pp; English.
XX
CC The present invention provides a method to prevent the transmission of
CC infectious agents during xenotransplantation. This involves introducing
CC to donor swine cells a recombinant DNA encoding a peptide fragment from
CC the infectious agent, and then introducing these cells into the
CC transplant recipient.
XX
SQ Sequence 21 BP; 1 A; 3 C; 8 G; 9 T; 0 other;

Query Match 64.0%; Score 12.8; DB 22; Length 21;
Best Local Similarity 87.5%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 gcggtgaccatgtagt 19
|||||| || ||||||
Db 5 gcggtgtccttgtagt 20

RESULT 13
AAA66374

ID AAA66374 standard; DNA; 24 BP.
XX
AC AAA66374;
XX
DT 09-OCT-2000 (first entry)
XX
DE Dog genomic marker oligonucleotide sequence SEQ ID NO:236.
XX
KW Dog; genome; genomic marker; radiation hybrid map; identification;
KW chromosome location; gene marker; polymorphic microsatellite marker;
KW phenotype; behaviour; pedigree; ss.
XX
OS Canis familiaris.
XX
PN WO200029615-A2.
XX
PD 25-MAY-2000.
XX
PF 15-NOV-1999; 99WO-IB01907.
XX
PR 13-NOV-1998; 98US-0108193.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Galibert F, Andre C;
XX
DR WPI; 2000-387821/33.
XX
PT New radiation hybrid map of the dog, Canine familiaris, genome, useful
PT for e.g. identifying genes implicated in phenotypic and behavioral
PT traits or in genetic diseases and for studying dog pedigrees -
XX
PS Claim 1; Page 63; 87pp; English.
XX
CC The present invention describes a radiation hybrid map of the dog
CC (Canine familiaris) genome comprising the genome location of a marker
CC selected from AAA66139 to AAA66942. The radiation hybrid map is useful
CC for identifying and localising dog genes, since it covers approximately
CC 80 % of the dog genome and provides a dense map integrating different
CC types (i.e. Type I and Type II) of markers. The map and the dog genome
CC markers (or complementary sequences) are especially useful to identify
CC genes responsible for phenotypic and behavioural traits in dogs, to
CC identify morbid genes, to analyse diseases and identify implicated genes
CC in such diseases and their alleles, and to study dog pedigrees. They
CC may also be useful for isolating corresponding human gene sequences
CC e.g. genes involved in genetic diseases.
XX
SQ Sequence 24 BP; 4 A; 6 C; 7 G; 7 T; 0 other;

Query Match 64.0%; Score 12.8; DB 21; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 cggtgaccatgtagtc 20
| ||||||||||| |
Db 8 ctgtgaccatgtagac 23

RESULT 14
AAF31123/c
ID AAF31123 standard; DNA; 27 BP.
XX
AC AAF31123;
XX
DT 27-APR-2001 (first entry)
XX
DE Mutagenic primer #2 for human SAH.
XX
KW Analyte-binding enzyme; analyte analysis; mutagenic primer; ss.
XX
OS Homo sapiens.
XX
PN WO200102600-A2.
XX
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18057.
XX
PR 06-JUL-1999; 99US-0347878.
PR 06-DEC-1999; 99US-0457205.
XX
PA (GEAT) GEN ATOMICS.
XX
PI Yuan C;
XX
DR WPI; 2001-071583/08.
XX
PT Assaying method, useful for prognosis and diagnosis of disease,
PT comprises contacting sample with a mutant analyte-binding enzyme and
PT detecting binding -
XX
PS Example 1; Page 151; 187pp; English.
XX
CC The present invention relates to a method for assaying an analyte in a
CC sample comprising: contacting the sample with a mutant analyte-binding
CC enzyme which has binding affinity for the analyte or an immediate
CC analyte enzymatic conversion product but has attenuated catalytic
CC activity; and detecting resulting binding. The method is useful in
CC monitoring biological systems/processes, or prognosis/diagnosis of
CC disease caused by imbalances of the analytes. The present sequence is
CC a mutagenic primer used in the present invention.
XX
SQ Sequence 27 BP; 5 A; 8 C; 8 G; 6 T; 0 other;

Query Match 64.0%; Score 12.8; DB 22; Length 27;
Best Local Similarity 87.5%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ctggcggtgaccatgt 16
||||||||||| | ||
Db 17 CTGGCGGTGACGAAGT 2

RESULT 15
AAV40536/c
ID AAV40536 standard; cDNA; 29 BP.
XX
AC AAV40536;
XX
DT 27-OCT-1998 (first entry)
XX
DE Homo sapiens CZ268_1 clone probe.
XX
KW secreted protein; CZ268_1; probe; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9830695-A2.
XX
PD 16-JUL-1998.
XX
PF 09-JAN-1998; 98WO-US00543.
XX
PR 08-JAN-1998; 98US-0004684.
PR 09-JAN-1997; 97US-0780814.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Agostino MJ, Jacobs K, Lavallie ER, Mccoy JM, Merberg D;
PI Racie LA, Spaulding V, Treacy M;
XX
DR WPI; 1998-413686/35.
XX

PT New isolated nucleic acids and secreted proteins - obtained from
PT human adult ovary, human foetal kidney, human foetal brain and human
PT adult brain cDNA libraries
XX
PS Disclosure; Page 97; 113pp; English.
XX
CC The sequence is that of a probe used to isolate a clone encoding
CC a novel secreted protein.
XX
SQ Sequence 29 BP; 5 A; 8 C; 7 G; 8 T; 1 other;

Query Match 64.0%; Score 12.8; DB 19; Length 29;
Best Local Similarity 82.4%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       1 ctggcggtgaccatgta 17
           |||| |||||||| | |
Db      17 CTGGAGGTGACCAAGNA 1
```

Search completed: March 13, 2002, 10:55:15
Job time: 3862 sec

Search completed: March 13, 2002, 10:55:17
Job time: 3864 sec

```
CC   the present invention.
XX
SQ   Sequence 58 BP; 20 A; 17 C; 6 G; 15 T; 0 other;


  Query Match           69.0%;  Score 13.8;  DB 21;  Length 58;
  Best Local Similarity  88.2%;  Pred. No. 8.5e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 aagtaggttgatgcttc 20
          |||| ||||| ||||||
Db     46 AAGTTGGTTGCTGCTTC 30


RESULT  14
AAC99528/c
ID   AAC99528 standard; DNA; 58 BP.
XX
AC   AAC99528;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human serum albumin (HSA) related oligonucleotide E-10.
XX
KW   Human serum albumin; HSA; ss.
XX
OS   Homo sapiens.
XX
PN   CN1266100-A.
XX
PD   13-SEP-2000.
XX
PF   04-MAR-1999;   99CN-0102794.
XX
PR   04-MAR-1999;   99CN-0102794.
XX
PA   (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI   Liu Z;
XX
DR   WPI; 2000-673207/66.
XX
PT   Novel methods for the chemical synthesis, expression and recombinant
PT   protein production for human serum albumin reformed gene -
XX
PS   Example 2; Fig 8; 85pp; Chinese.
XX
CC   The present invention relates to two kinds of DNA sequences of coded
CC   human serum albumin (HSA), i.e. design of structure-modified gene
CC   segment of HSA and artificial total synthesis and a production process
CC   for large-scale production of genetic recombinant HSA by using
CC   methanol, yeast and engineering bacterium, and discovers that the
CC   structure-modified gene can greatly increase the expression quantity
CC   of HSA. The production process can make the structural gene of HSA
CC   obtain high-level expression under the drive of promoter induced by
CC   methanol, and make the HSA expression product secrete into the
CC   fermenting liquor culture medium, and provide reliable test data for
CC   more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC   to AAC99391 represent oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 58 BP; 20 A; 17 C; 6 G; 15 T; 0 other;


  Query Match           69.0%;  Score 13.8;  DB 21;  Length 58;
  Best Local Similarity  88.2%;  Pred. No. 8.5e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 aagtaggttgatgcttc 20
          |||| ||||| ||||||
Db     46 AAGTTGGTTGCTGCTTC 30


RESULT  15
AAZ96982
ID   AAZ96982 standard; DNA; 59 BP.
XX
AC   AAZ96982;
XX
DT   14-APR-2000  (first entry)
XX
DE   S. cerevisiae gene deletion cassette constructing primer YDR181c-S1.
XX
KW   Antimycotic; mycosis; immunodepression; AIDS; diabetes; fungicide;
KW   mycete; gene deletion; PCR primer; ss.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO9955907-A2.
XX
PD   04-NOV-1999.
XX
PF   22-APR-1999;   99WO-EP02722.
XX
PR   24-APR-1998;   98EP-0401007.
PR   11-SEP-1998;   98EP-0402254.
XX
PA   (HMRI ) HOECHST MARION ROUSSEL.
XX
PI   Diu-Hercend A,  Entian K,  Koetter P;
XX
DR   WPI; 2000-105527/09.
XX
PT   Identifying antimycotic substances useful for drug preparation and
PT   treatment of mycosis -
XX
PS   Examples; Page 84; 86pp; English.
XX
CC   The invention provides a method of screening for antimycotic substances
CC   using essential genes from mycetes or a functionally similar mycete
CC   gene or the corresponding encoded protein as target. The essential gene
CC   useful for screening antimycotic substances is selected from the
CC   following genes: YML114c, YLR186w, YLR215c, YLR222c, YLR243w, YLR272c,
CC   YLR275w, YLR276c, YLR317w, YLR359w, YLR373c, YLR424w, YLR437c, YLR440c,
CC   YML023c, YML049c, YML077w, YML093w, YML127w, YMR032w, YMR093w, YMR131c,
CC   YMR185w, YMR212c, YMR213w, YMR218c, YMR281w, YMR288w, YMR290c, YMR211w,
CC   YMR049c, YMR134w, YDR196c, YDR299w, YDR365c, YDR396w, YDR407c, YDR416w,
CC   YDR449c, YDR472w, YDR499w, YDR141c, YDR324c, YDR325w, YDR398w, YDR246w,
CC   YDR236c, YDR361c, YDR367w, YDR339c, YDR413c, YDR429c, YDR468c, YDR489w,
CC   YDR527w, YDR288w, YDR201w, YDR434w, YDR181c, YDR531w, YPL126w, YPL093w,
CC   YPL063w, YPL024w, YPL020c, YPL012w, YPL007c, YPL233w, YPL146c, YIL091c,
CC   YIL083c, YIL019w, YIL109c, YIL104c, YFL024c, YFR003c, YFR027w, YFR042w,
CC   YIR010w, YIR015w, YPR048w, YPR072w, YPR082c, YPR085c, YPR105c, YPR112c,
CC   YPR137w, YPR143w, YPR144c and YPR169w. The method is useful for
CC   identifying substances for the preparation of drugs for the treatment of
CC   mycosis or prevention in immunodepression states. Drugs containing
CC   antimycotic substances are useful for the treatment of mycotic
CC   infections which occur during diseases like AIDS or diabetes. Substances
CC   which may be used for the fabrication of fungicides, especially of
CC   fungicides which are harmless for humans and animals and antimycotic
CC   substances which selectively inhibit the growth of specific mycete
CC   species only, can also be identified by this method. Sequences
CC   AAZ96811-Z96990 represent PCR primers used in construction of S.
CC   cerevisiae deletion cassettes.
XX
SQ   Sequence 59 BP; 21 A; 13 C; 13 G; 12 T; 0 other;


  Query Match           68.0%;  Score 13.6;  DB 21;  Length 59;
  Best Local Similarity  80.0%;  Pred. No. 1.1e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 tctaagtaggttgatgcttc 20
          ||||||| | ||| |||||
Db     34 tctaagtcagctgaagcttc 53
```

PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
XX
DR WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer -
XX
PS Claim 5; Page 172; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 54 BP; 23 A; 17 C; 9 G; 5 T; 0 other;

Query Match 69.0%; Score 13.8; DB 22; Length 54;
Best Local Similarity 88.2%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 aagtaggttgatgcttc 20
|||| | ||||||||||
Db 40 AAGTGGATTGATGCTTC 24

RESULT 12
AAH02544/c
ID AAH02544 standard; cDNA; 54 BP.
XX
AC AAH02544;
XX
DT 14-JUN-2001 (first entry)
XX
DE Prostate tumour antigen determined cDNA sequence for P126.
XX
KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
KW prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200125272-A2.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000WO-US27464.
XX
PR 04-OCT-1999; 99US-0157455.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Skeiky YAW, Reed SG, Cheever MA;
XX
DR WPI; 2001-245062/25.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer -
XX
PS Claim 4; Page 162; 276pp; English.
XX
CC The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 54 BP; 23 A; 17 C; 9 G; 5 T; 0 other;

Query Match 69.0%; Score 13.8; DB 22; Length 54;
Best Local Similarity 88.2%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 aagtaggttgatgcttc 20
|||| | ||||||||||
Db 40 AAGTGGATTGATGCTTC 24

RESULT 13
AAC99381/c
ID AAC99381 standard; DNA; 58 BP.
XX
AC AAC99381;
XX
DT 07-MAR-2001 (first entry)
XX
DE Human serum albumin (HSA) related oligonucleotide E-10.
XX
KW Human serum albumin; HSA; ss.
XX
OS Homo sapiens.
XX
PN CN1266099-A.
XX
PD 13-SEP-2000.
XX
PF 04-MAR-1999; 99CN-0102745.
XX
PR 04-MAR-1999; 99CN-0102745.
XX
PA (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI Liu Z;
XX
DR WPI; 2000-673206/66.
XX
PT Novel methods for chemical synthesis, expression and recombinant
PT protein production for human serum albumin reformed gene -
XX
PS Example 2; Fig 8; 85pp; Chinese.
XX
CC The present invention relates to two kinds of DNA sequences of coded
CC human serum albumin (HSA), i.e. design of structure-modified gene
CC segment of HSA and artificial total synthesis and a production process
CC for large-scale production of genetic recombinant HSA by using
CC methanol, yeast and engineering bacterium, and discovers that the
CC structure-modified gene can greatly increase the expression quantity
CC of HSA. The production process can make the structural gene of HSA
CC obtain high-level expression under the drive of promoter induced by
CC methanol, and make the HSA expression product secrete into the
CC fermenting liquor culture medium, and provide reliable test data for
CC more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC to AAC99391 represent oligonucleotides used in the exemplification of

```
  Best Local Similarity   88.2%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 aagtaggttgatgcttc 20
           |||| | ||||||||||
Db      40 AAGTGGATTGATGCTTC 24


RESULT   9
AAS10122/c
ID   AAS10122 standard; cDNA; 54 BP.
XX
AC   AAS10122;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human prostate tumour cDNA #13.
XX
KW   Human; prostate tumour protein; prostate cancer; ss.
XX
OS   Homo sapiens.
XX
PN   US6262245-B1.
XX
PD   17-JUL-2001.
XX
PF   25-FEB-1998;   98US-0030607.
XX
PR   25-FEB-1997;   97US-0806099.
PR   01-AUG-1997;   97US-0904804.
PR   09-FEB-1998;   98US-0020956.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J,  Dillon DC;
XX
DR   WPI; 2001-440862/47.
XX
PT   Novel polynucleotide encoding polypeptide comprising a portion of
PT   prostate tumour protein useful for inhibiting development of prostate
PT   cancer or for treating prostate cancer in a patient  -
XX
PS   Example 2; Column 137; 105pp; English.
XX
CC   The sequence is a human prostate tumour cDNA which encodes a
CC   partial tumour protein. The DNA is useful for inhibiting the development
CC   of prostate cancer or for treating prostate cancer in a patient.
XX
SQ   Sequence 54 BP; 23 A; 17 C; 9 G; 5 T; 0 other;


  Query Match           69.0%;  Score 13.8;  DB 22;  Length 54;
  Best Local Similarity   88.2%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 aagtaggttgatgcttc 20
           |||| | ||||||||||
Db      40 AAGTGGATTGATGCTTC 24


RESULT  10
AAH93479/c
ID   AAH93479 standard; cDNA; 54 BP.
XX
AC   AAH93479;
XX
DT   04-OCT-2001  (first entry)
XX
DE   Human prostate-specific cDNA sequence P126.
XX
KW   Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW   cytostatic; gene therapy; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200151633-A2.
XX
PD   19-JUL-2001.
XX
PF   16-JAN-2001; 2001WO-US01574.
XX
PR   14-JAN-2000; 2000US-0483672.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J,  Dillon DC,  Mitcham JL,  Harlocker SL,  Jiang Y,  Reed SG;
PI   Kalos MD,  Fanger GR,  Day CH,  Retter MW,  Stolk JA,  Skeiky YAW;
PI   Wang A,  Meagher MJ;
XX
DR   WPI; 2001-425873/45.
XX
PT   New polynucleotide encoding a prostate-specific protein, for
PT   diagnosing, monitoring and treating prostate cancer in a patient and
PT   for use in vaccines -
XX
PS   Claim 1; Page 272; 543pp; English.
XX
CC   The present invention describes polynucleotide sequences (I) which encode
CC   prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC   and can be used in vaccine production and gene therapy. (I), (II),
CC   antibodies to (II), fusion proteins comprising (II), and isolated
CC   T cells prepared using (I) or (II) are used treat cancer in a patient.
CC   (I) and the antibodies are also used in the detection of cancer in a
CC   patient. The cancer that is diagnosed or treated is particularly
CC   prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC   (I) can be used for monitoring the progression of cancer in a patient.
CC   (I) and (II) can also be used to improve diagnostic and therapeutic
CC   methods for prostate cancer. They can indicate the level of metastasis
CC   as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to
CC   AAM01318 represent polynucleotide and amino acid sequences used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 54 BP; 23 A; 17 C; 9 G; 5 T; 0 other;


  Query Match           69.0%;  Score 13.8;  DB 22;  Length 54;
  Best Local Similarity   88.2%;  Pred. No. 8.4e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 aagtaggttgatgcttc 20
           |||| | ||||||||||
Db      40 AAGTGGATTGATGCTTC 24


RESULT  11
AAH84793/c
ID   AAH84793 standard; cDNA; 54 BP.
XX
AC   AAH84793;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Human prostate-specific cDNA sequence P126.
XX
KW   Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW   chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW   prostate specific antigen; PSA; ss.
XX
OS   Homo sapiens.
XX
PN   WO200134802-A2.
XX
PD   17-MAY-2001.
XX
PF   09-NOV-2000; 2000WO-US30904.
XX
```

PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
DR WPI; 1998-609886/51.
XX
PT Polypeptides comprising immunogenic portions of prostate proteins -
PT used in a vaccine for the treatment of prostate cancer
XX
PS Claim 3; Page 89; 130pp; English.
XX
CC The present sequence is a new DNA which encodes an immunogenic portion
CC of a prostate tumour protein. The encoded immunogen, or the DNA itself,
CC can be used as a vaccine for the treatment of prostate cancer. The DNA
CC was identified by analysis of a subtracted cDNA library obtained by
CC subtracting a prostate tumour cDNA expression library with a normal
CC tissue cDNA library.
XX
SQ Sequence 54 BP; 23 A; 17 C; 9 G; 5 T; 0 other;

Query Match 69.0%; Score 13.8; DB 19; Length 54;
Best Local Similarity 88.2%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 aagtaggttgatgcttc 20
|||| | ||||||||||
Db 40 AAGTGGATTGATGCTTC 24

RESULT 7
AAV58600/c
ID AAV58600 standard; cDNA; 54 BP.
XX
AC AAV58600;
XX
DT 08-DEC-1998 (first entry)
XX
DE Prostate tumour specific gene clone.
XX
KW Prostate tumour specific gene; human; prostate cancer; detection;
KW therapy; ss.
XX
OS Homo sapiens.
XX
PN WO9837418-A2.
XX
PD 27-AUG-1998.
XX
PF 25-FEB-1998; 98WO-US03690.
XX
PR 09-FEB-1998; 98US-0904809.
PR 25-FEB-1997; 97US-0806596.
PR 01-AUG-1997; 97US-0904809.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Xu J;
XX
DR WPI; 1998-480805/41.
XX
PT Novel human prostate specific tumour protein and fragments - useful
PT for detecting and treating prostate cancers
XX
PS Claim 1; Page 95; 141pp; English.
XX
CC This sequence represents a human prostate tumour specific gene, and can
CC be used in the method of the invention. The method is for detecting
CC prostate cancer comprises contacting a biological sample with an agent
CC able to bind an immunogenic portion of a prostate protein (such as
CC encoded by this sequence). An antibody which binds to an immunogenic
CC portion of the prostate protein, and the method can be used to detect,
CC monitor progression of, or treat prostate cancers. The antibody may
CC also be conjugated to a therapeutic agent for use in therapy of prostate
CC cancers.
XX
SQ Sequence 54 BP; 23 A; 17 C; 9 G; 5 T; 0 other;

Query Match 69.0%; Score 13.8; DB 19; Length 54;
Best Local Similarity 88.2%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 aagtaggttgatgcttc 20
|||| | ||||||||||
Db 40 AAGTGGATTGATGCTTC 24

RESULT 8
AAA06363/c
ID AAA06363 standard; cDNA; 54 BP.
XX
AC AAA06363;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:127.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
XX
DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
PS Claim 1; Page 143; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AAY82000 to AAY82020 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 54 BP; 23 A; 17 C; 9 G; 5 T; 0 other;

Query Match 69.0%; Score 13.8; DB 21; Length 54;

```
          |||||| |||||||||
Db     18 AGTAGGATGATGCTTC 3


RESULT   4
AAC99380
ID   AAC99380 standard; DNA; 45 BP.
XX
AC   AAC99380;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human serum albumin (HSA) related oligonucleotide E-9.
XX
KW   Human serum albumin; HSA; ss.
XX
OS   Homo sapiens.
XX
PN   CN1266099-A.
XX
PD   13-SEP-2000.
XX
PF   04-MAR-1999;   99CN-0102745.
XX
PR   04-MAR-1999;   99CN-0102745.
XX
PA   (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI   Liu Z;
XX
DR   WPI; 2000-673206/66.
XX
PT   Novel methods for chemical synthesis, expression and recombinant
PT   protein production for human serum albumin reformed gene -
XX
PS   Example 2; Fig 8; 85pp; Chinese.
XX
CC   The present invention relates to two kinds of DNA sequences of coded
CC   human serum albumin (HSA), i.e. design of structure-modified gene
CC   segment of HSA and artificial total synthesis and a production process
CC   for large-scale production of genetic recombinant HSA by using
CC   methanol, yeast and engineering bacterium, and discovers that the
CC   structure-modified gene can greatly increase the expression quantity
CC   of HSA. The production process can make the structural gene of HSA
CC   obtain high-level expression under the drive of promoter induced by
CC   methanol, and make the HSA expression product secrete into the
CC   fermenting liquor culture medium, and provide reliable test data for
CC   more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC   to AAC99391 represent oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 45 BP; 9 A; 6 C; 13 G; 17 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 21;  Length 45;
  Best Local Similarity   88.2%;  Pred. No. 8.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 aagtaggttgatgcttc 20
          |||| ||||| ||||||
Db      4 aagttggttgctgcttc 20


RESULT   5
AAC99527
ID   AAC99527 standard; DNA; 45 BP.
XX
AC   AAC99527;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human serum albumin (HSA) related oligonucleotide E-9.
XX
KW   Human serum albumin; HSA; ss.
XX
OS   Homo sapiens.
XX
PN   CN1266100-A.
XX
PD   13-SEP-2000.
XX
PF   04-MAR-1999;   99CN-0102794.
XX
PR   04-MAR-1999;   99CN-0102794.
XX
PA   (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI   Liu Z;
XX
DR   WPI; 2000-673207/66.
XX
PT   Novel methods for the chemical synthesis, expression and recombinant
PT   protein production for human serum albumin reformed gene -
XX
PS   Example 2; Fig 8; 85pp; Chinese.
XX
CC   The present invention relates to two kinds of DNA sequences of coded
CC   human serum albumin (HSA), i.e. design of structure-modified gene
CC   segment of HSA and artificial total synthesis and a production process
CC   for large-scale production of genetic recombinant HSA by using
CC   methanol, yeast and engineering bacterium, and discovers that the
CC   structure-modified gene can greatly increase the expression quantity
CC   of HSA. The production process can make the structural gene of HSA
CC   obtain high-level expression under the drive of promoter induced by
CC   methanol, and make the HSA expression product secrete into the
CC   fermenting liquor culture medium, and provide reliable test data for
CC   more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC   to AAC99391 represent oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 45 BP; 9 A; 6 C; 13 G; 17 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 21;  Length 45;
  Best Local Similarity   88.2%;  Pred. No. 8.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 aagtaggttgatgcttc 20
          |||| ||||| ||||||
Db      4 aagttggttgctgcttc 20


RESULT   6
AAV61215/c
ID   AAV61215 standard; cDNA; 54 BP.
XX
AC   AAV61215;
XX
DT   06-JAN-1999  (first entry)
XX
DE   cDNA sequence of prostate tumour clone.
XX
KW   Prostate; cancer; tumour; vaccine; immunogen; clone; ss.
XX
OS   Homo sapiens.
XX
PN   WO9837093-A2.
XX
PD   27-AUG-1998.
XX
PF   25-FEB-1998;   98WO-US03492.
XX
PR   09-FEB-1998;   98US-0020956.
PR   25-FEB-1997;   97US-0806099.
PR   01-AUG-1997;   97US-0904804.
XX
```

XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 3; Page 720; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 13 A; 8 C; 5 G; 21 T; 0 other;

Query Match 77.0%; Score 15.4; DB 21; Length 47;
Best Local Similarity 94.1%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tctaagtaggttgatgc 17
| ||||||||||||||||
Db 20 TTTAAGTAGGTTGATGC 4

RESULT 2
AAQ91630
ID AAQ91630 standard; DNA; 33 BP.
XX
AC AAQ91630;
XX
DT 06-FEB-1996 (first entry)
XX
DE Human apolipoprotein (a) (apo(a)) C-terminal primer 91.
XX
KW Human; old world monkey; apolipoprotein (a); apo(a); primer 91;
KW detection; quantification; C-terminal; ss.
XX
OS Synthetic.
XX
PN EP659765-A2.
XX
PD 28-JUN-1995.
XX
PF 16-DEC-1994; 94EP-0203653.
XX
PR 27-JUN-1994; 94US-0266407.
PR 21-DEC-1993; 93US-0172461.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Butler SM, Taddei-peters WC;
XX
DR WPI; 1995-226203/30.
XX
PT New immuno:reactive peptide(s) of apo:lipoprotein - used for prodn.
PT of antibodies and development of immunoassays, for the detection and
PT quantification of apo(a)
XX
PS Claim 19; Page 11; 44pp; English.
XX
CC AAQ91630 is the human/old world monkey apolipoprotein (a) (apo(a))
CC C-terminal primer 91. It was used for the C-terminal mapping
CC of amplified apo(a) DNA prods.. The primer can also be used as a
CC probe for the detection, and quantification of apo(a) DNA.
XX
SQ Sequence 33 BP; 6 A; 7 C; 10 G; 10 T; 0 other;

Query Match 75.0%; Score 15; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 gtaggttgatgcttc 20
||||||||||||||||
Db 13 gtaggttgatgcttc 27

RESULT 3
AAX92137/c
ID AAX92137 standard; DNA; 20 BP.
XX
AC AAX92137;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydia pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB01890.
XX
PR 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae
XX
PS Page 1488; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading
CC frames and other nucleic acid sequences from the genome of
CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
CC disease such as pneumonia and bronchitis and is thought to be a
CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC by the open reading frames of the C. pneumoniae genome (see AAY34584-
CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC containing C. pneumoniae nucleotides sequences can also be used as
CC immunogenic compositions, especially where the vector directs the
CC expression of a neutralising epitope of C. pneumoniae.
XX
SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 other;

Query Match 72.0%; Score 14.4; DB 20; Length 20;
Best Local Similarity 93.8%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 agtaggttgatgcttc 20

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 10:55:15 ; Search time 968.42 Seconds
(without alignments)
17.706 Million cell updates/sec

Title: US-09-923-515-35
Perfect score: 20
Sequence: 1 tctaagtaggttgatgcttc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	15.4	77.0	47	21	AAZ67950	Human map-related
	2	15	75.0	33	16	AAQ91630	Human apolipoprote
c	3	14.4	72.0	20	20	AAX92137	PCR primer used to
	4	13.8	69.0	45	21	AAC99380	Human serum albumi
	5	13.8	69.0	45	21	AAC99527	Human serum albumi
c	6	13.8	69.0	54	19	AAV61215	cDNA sequence of p
c	7	13.8	69.0	54	19	AAV58600	Prostate tumour sp
c	8	13.8	69.0	54	21	AAA06363	Human immunogenic
c	9	13.8	69.0	54	22	AAS10122	Human prostate tum
c	10	13.8	69.0	54	22	AAH93479	Human prostate-spe
c	11	13.8	69.0	54	22	AAH84793	Human prostate-spe
c	12	13.8	69.0	54	22	AAH02544	Prostate tumour an
c	13	13.8	69.0	58	21	AAC99381	Human serum albumi
c	14	13.8	69.0	58	21	AAC99528	Human serum albumi
	15	13.6	68.0	59	21	AAZ96982	S. cerevisiae gene
	16	13.4	67.0	41	19	AAV51071	Maize polymorphic
	17	13.4	67.0	41	19	AAV51078	Maize polymorphic
c	18	13.4	67.0	50	18	AAV76408	Staphylococcus aur
	19	13.2	66.0	47	21	AAZ67270	Human map-related
	20	13	65.0	41	19	AAV47826	Maize polymorphic
	21	13	65.0	41	19	AAV47819	Maize polymorphic
	22	12.8	64.0	52	20	AAX52316	Probe used to isol
	23	12.8	64.0	52	22	AAF72474	Human PRO polypept
c	24	12.6	63.0	32	21	AAC63828	G protein-inducibl
c	25	12.6	63.0	32	21	AAZ44381	Human G protein-co
	26	12.6	63.0	34	19	AAV24015	PCR primer for hum
c	27	12.6	63.0	56	17	AAT10516	MI3 insulin precur
	28	12.4	62.0	56	21	AAA46580	PCR primer used to
c	29	12.2	61.0	19	22	AAF94774	Rac 1 antisense ph
	30	12.2	61.0	20	20	AAZ40470	Primer #2 for Mimu
	31	12.2	61.0	24	22	AAH23733	Threonine syntheta
	32	12.2	61.0	25	21	AAA68589	Bacteriophage 3A O
	33	12.2	61.0	27	21	AAA60911	Coprinus cinereus
	34	12.2	61.0	35	21	AAC63504	Oestrogen receptor
	35	12.2	61.0	35	22	AAH57123	Human androgen rec
c	36	12.2	61.0	47	21	AAZ66836	Human map-related
	37	12	60.0	24	19	AAV11381	Plasmid p35S GUS I
	38	12	60.0	24	19	AAV10417	S. cerevisiae acet
c	39	12	60.0	28	18	AAT72924	Treponema pallidum
	40	12	60.0	35	13	AAQ29318	PCR primer JAT33 f
	41	12	60.0	35	16	AAQ81601	Plasmodium falcipa
	42	12	60.0	44	19	AAV49665	Human J chain targ
	43	12	60.0	44	20	AAX08808	DNA sequence encod
c	44	12	60.0	47	21	AAA99022	H. influenzae adhe
	45	12	60.0	47	21	AAA99023	H. influenzae adhe

ALIGNMENTS

RESULT 1
AAZ67950/c
ID AAZ67950 standard; DNA; 47 BP.
XX
AC AAZ67950;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:2297.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,A)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 09:50:41 ; Search time 1263.07 Seconds
(without alignments)
13.575 Million cell updates/sec

Title: US-09-923-515-24
Perfect score: 20
Sequence: 1 tgaccaagcttggcaagttc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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12: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:*
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19: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		18.4	92.0	26	20	AAX89305	Primer used in RT-
2		15.8	79.0	49	21	AAC99322	Human serum albumi
3		15.8	79.0	49	21	AAC99469	Human serum albumi
c 4		15.8	79.0	50	21	AAC99321	Human serum albumi
c 5		15.8	79.0	50	21	AAC99468	Human serum albumi
c 6		14.4	72.0	36	20	AAX36413	PCR primer for IFN
c 7		14.4	72.0	36	20	AAX16122	PCR primer used in
c 8		14.4	72.0	36	22	AAF25939	Canine gamma inter
9		14.2	71.0	33	19	AAV39953	Streptococcus pneu
10		13.8	69.0	21	22	AAF80319	PCR primer used to
11		13.8	69.0	23	19	AAV42325	Basidiomycete phyt
12		13.8	69.0	33	22	AAD02795	Candida albicans E
13		13.8	69.0	40	18	AAT61665	Antibody expressio
c 14		13.4	67.0	54	14	AAQ42332	Gamma globin gene
c 15		13.4	67.0	54	19	AAV08758	PCR primer GAM-3-H
c 16		13.4	67.0	54	22	AAF31402	Oligonucleotide.
17		13.2	66.0	24	18	AAT95660	Primer for SSCP an
18		13.2	66.0	24	19	AAV56557	Human DP2.5 APC pr
19		13.2	66.0	24	19	AAT96274	Primer for SSCP an
20		13.2	66.0	24	21	AAA93559	Human APC (DP2.5)
21		13.2	66.0	25	15	AAQ72560	Adenomatous polypo
22		13.2	66.0	51	16	AAT04229	Bovine histamine H
c 23		13	65.0	15	17	AAT37608	Apo(a) mRNA (nt. p
c 24		13	65.0	15	17	AAT37558	Apo(a) mRNA (nt. p
25		12.8	64.0	20	21	AAC86426	Wheat starch synth
c 26		12.8	64.0	20	21	AAC86427	Wheat starch synth
27		12.8	64.0	21	19	AAV53747	Nucleotide sequenc
28		12.8	64.0	25	18	AAT72089	Arabidopsis b1-tub
c 29		12.8	64.0	45	18	AAT61657	Chloramphenicol ac
c 30		12.6	63.0	33	22	AAF56429	Neisseria meningit
c 31		12.6	63.0	33	22	AAF56435	Neisseria meningit
c 32		12.6	63.0	35	21	AAC64260	Soybean cotyledon
33		12.6	63.0	36	16	AAT05466	Sequence encoding
34		12.6	63.0	48	20	AAZ00287	HEV specific prime
c 35		12.4	62.0	19	21	AAZ74006	Human biallelic ma
36		12.4	62.0	25	21	AAZ97493	HIV-1 protease gen
c 37		12.4	62.0	26	13	AAQ25288	PCR primer for Hin
c 38		12.4	62.0	26	13	AAQ31240	Factor IX targetti
c 39		12.4	62.0	26	16	AAQ76224	Primer for amplifi
c 40		12.4	62.0	26	18	AAV05341	PCR primer used to
c 41		12.4	62.0	26	18	AAT97338	Construction of ma
c 42		12.4	62.0	26	18	AAT58595	Cytomegalovirus im
c 43		12.4	62.0	26	18	AAT58620	Human cytomegalovi
c 44		12.4	62.0	26	20	AAV99465	PCR primer 9 used
c 45		12.4	62.0	26	20	AAV68116	PCR primer 9 used

ALIGNMENTS

RESULT 1
AAX89305
ID AAX89305 standard; DNA; 26 BP.
XX
AC AAX89305;
XX
DT 21-SEP-1999 (first entry)
XX
DE Primer used in RT-PCR analysis of transgenic apo(a).
XX
KW Transgenic rabbit; apolipoprotein (a); apolipoprotein B; lipoprotein;
KW atherosclerotic lesion; cholesterol; vascular injury; restenosis; apoB;
KW RT-PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9935241-A1.
XX
PD 15-JUL-1999.
XX
PF 08-JAN-1999; 99WO-US00401.
XX
PR 08-JAN-1998; 98US-0070727.
XX
PA (RHON) RHONE-POULENC RORER PHARM INC.
XX
PI Denefle P, Duverger N, Emmanuel F, Houdebine L;
PI Hughes SD, Rouy D, Rubin E, Viglietta C;
XX
DR WPI; 1999-430386/36.
XX
PT A transgenic rabbit that expresses a functional human lipoprotein A
XX
PS Example 3; Page 46; 73pp; English.

```
XX
CC   The invention provides a transgenic rabbit, which has in its genomic
CC   DNA, sequences that encode apolipoprotein (a) and apolipoprotein B
CC   polypeptides, which are capable of combining to produce lipoprotein (a).
CC   The transgenic rabbit expresses a functional human lipoprotein (a). The
CC   rabbit develops human-like atherosclerotic lesions when fed a
CC   cholesterol rich diet. The transgenic rabbit is useful as a model for
CC   human diseases that are induced and/or exacerbated by lipoprotein (a)
CC   expression. The model can be used to identify inhibitors of lipoprotein
CC   (a) particle assembly and inhibitors of lipoprotein (a) associated
CC   diseases. The rabbit model is advantageous, when compared to the mouse,
CC   due partly to its relatively larger size, enabling facile studies of
CC   vascular injury and restenosis. In addition, while rabbits are similar to
CC   mice in lacking apo(a) and lipoprotein (a), their lipoprotein profile
CC   more closely mimics that of humans, with LDL as the predominant plasma
CC   lipoprotein. Sequences AAX89305-308 represent priomers used in the
CC   analysisi of transgenic apo(a) and apoB.
XX
SQ   Sequence 26 BP; 5 A; 7 C; 7 G; 7 T; 0 other;


  Query Match             92.0%;  Score 18.4;  DB 20;  Length 26;
  Best Local Similarity   95.0%;  Pred. No. 4.7;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 tgaccaagcttggcaagttc 20
           |||||||||||||||| ||||
Db       3 tgaccaagcttggcaggttc 22


RESULT   2
AAC99322
ID   AAC99322 standard; DNA; 49 BP.
XX
AC   AAC99322;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human serum albumin (HSA) related oligonucleotide A-9.
XX
KW   Human serum albumin; HSA; ss.
XX
OS   Homo sapiens.
XX
PN   CN1266099-A.
XX
PD   13-SEP-2000.
XX
PF   04-MAR-1999;   99CN-0102745.
XX
PR   04-MAR-1999;   99CN-0102745.
XX
PA   (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI   Liu Z;
XX
DR   WPI; 2000-673206/66.
XX
PT   Novel methods for chemical synthesis, expression and recombinant
PT   protein production for human serum albumin reformed gene -
XX
PS   Example 2; Fig 8; 85pp; Chinese.
XX
CC   The present invention relates to two kinds of DNA sequences of coded
CC   human serum albumin (HSA), i.e. design of structure-modified gene
CC   segment of HSA and artificial total synthesis and a production process
CC   for large-scale production of genetic recombinant HSA by using
CC   methanol, yeast and engineering bacterium, and discovers that the
CC   structure-modified gene can greatly increase the expression quantity
CC   of HSA. The production process can make the structural gene of HSA
CC   obtain high-level expression under the drive of promoter induced by
CC   methanol, and make the HSA expression product secrete into the
CC   fermenting liquor culture medium, and provide reliable test data for
CC   more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC   to AAC99391 represent oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 49 BP; 7 A; 11 C; 12 G; 19 T; 0 other;


  Query Match             79.0%;  Score 15.8;  DB 21;  Length 49;
  Best Local Similarity   89.5%;  Pred. No. 96;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tgaccaagcttggcaagtt 19
           | ||||| ||||||||||
Db      14 taaccaatcttggcaagtt 32


RESULT   3
AAC99469
ID   AAC99469 standard; DNA; 49 BP.
XX
AC   AAC99469;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human serum albumin (HSA) related oligonucleotide A-9.
XX
KW   Human serum albumin; HSA; ss.
XX
OS   Homo sapiens.
XX
PN   CN1266100-A.
XX
PD   13-SEP-2000.
XX
PF   04-MAR-1999;   99CN-0102794.
XX
PR   04-MAR-1999;   99CN-0102794.
XX
PA   (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI   Liu Z;
XX
DR   WPI; 2000-673207/66.
XX
PT   Novel methods for the chemical synthesis, expression and recombinant
PT   protein production for human serum albumin reformed gene -
XX
PS   Example 2; Fig 8; 85pp; Chinese.
XX
CC   The present invention relates to two kinds of DNA sequences of coded
CC   human serum albumin (HSA), i.e. design of structure-modified gene
CC   segment of HSA and artificial total synthesis and a production process
CC   for large-scale production of genetic recombinant HSA by using
CC   methanol, yeast and engineering bacterium, and discovers that the
CC   structure-modified gene can greatly increase the expression quantity
CC   of HSA. The production process can make the structural gene of HSA
CC   obtain high-level expression under the drive of promoter induced by
CC   methanol, and make the HSA expression product secrete into the
CC   fermenting liquor culture medium, and provide reliable test data for
CC   more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC   to AAC99391 represent oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 49 BP; 7 A; 11 C; 12 G; 19 T; 0 other;


  Query Match             79.0%;  Score 15.8;  DB 21;  Length 49;
  Best Local Similarity   89.5%;  Pred. No. 96;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tgaccaagcttggcaagtt 19
           | ||||| ||||||||||
Db      14 taaccaatcttggcaagtt 32
```

RESULT 4
AAC99321/c
ID AAC99321 standard; DNA; 50 BP.
XX
AC AAC99321;
XX
DT 07-MAR-2001 (first entry)
XX
DE Human serum albumin (HSA) related oligonucleotide A-8.
XX
KW Human serum albumin; HSA; ss.
XX
OS Homo sapiens.
XX
PN CN1266099-A.
XX
PD 13-SEP-2000.
XX
PF 04-MAR-1999; 99CN-0102745.
XX
PR 04-MAR-1999; 99CN-0102745.
XX
PA (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI Liu Z;
XX
DR WPI; 2000-673206/66.
XX
PT Novel methods for chemical synthesis, expression and recombinant
PT protein production for human serum albumin reformed gene -
XX
PS Example 2; Fig 8; 85pp; Chinese.
XX
CC The present invention relates to two kinds of DNA sequences of coded
CC human serum albumin (HSA), i.e. design of structure-modified gene
CC segment of HSA and artificial total synthesis and a production process
CC for large-scale production of genetic recombinant HSA by using
CC methanol, yeast and engineering bacterium, and discovers that the
CC structure-modified gene can greatly increase the expression quantity
CC of HSA. The production process can make the structural gene of HSA
CC obtain high-level expression under the drive of promoter induced by
CC methanol, and make the HSA expression product secrete into the
CC fermenting liquor culture medium, and provide reliable test data for
CC more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC to AAC99391 represent oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 50 BP; 20 A; 13 C; 11 G; 6 T; 0 other;

Query Match 79.0%; Score 15.8; DB 21; Length 50;
Best Local Similarity 89.5%; Pred. No. 96;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgaccaagcttggcaagtt 19
| ||||| ||||||||||
Db 41 TAACCAATCTTGGCAAGTT 23

RESULT 5
AAC99468/c
ID AAC99468 standard; DNA; 50 BP.
XX
AC AAC99468;
XX
DT 07-MAR-2001 (first entry)
XX
DE Human serum albumin (HSA) related oligonucleotide A-8.
XX
KW Human serum albumin; HSA; ss.
XX
OS Homo sapiens.
XX
PN CN1266100-A.
XX
PD 13-SEP-2000.
XX
PF 04-MAR-1999; 99CN-0102794.
XX
PR 04-MAR-1999; 99CN-0102794.
XX
PA (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI Liu Z;
XX
DR WPI; 2000-673207/66.
XX
PT Novel methods for the chemical synthesis, expression and recombinant
PT protein production for human serum albumin reformed gene -
XX
PS Example 2; Fig 8; 85pp; Chinese.
XX
CC The present invention relates to two kinds of DNA sequences of coded
CC human serum albumin (HSA), i.e. design of structure-modified gene
CC segment of HSA and artificial total synthesis and a production process
CC for large-scale production of genetic recombinant HSA by using
CC methanol, yeast and engineering bacterium, and discovers that the
CC structure-modified gene can greatly increase the expression quantity
CC of HSA. The production process can make the structural gene of HSA
CC obtain high-level expression under the drive of promoter induced by
CC methanol, and make the HSA expression product secrete into the
CC fermenting liquor culture medium, and provide reliable test data for
CC more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC to AAC99391 represent oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 50 BP; 20 A; 13 C; 11 G; 6 T; 0 other;

Query Match 79.0%; Score 15.8; DB 21; Length 50;
Best Local Similarity 89.5%; Pred. No. 96;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgaccaagcttggcaagtt 19
| ||||| ||||||||||
Db 41 TAACCAATCTTGGCAAGTT 23

RESULT 6
AAX36413/c
ID AAX36413 standard; DNA; 36 BP.
XX
AC AAX36413;
XX
DT 06-JUL-1999 (first entry)
XX
DE PCR primer for IFN-gamma coding sequence.
XX
KW Interferon-gamma; IFN-gamma; recombinant baculovirus; silkworm larvae;
KW IFN-gamma production; PCR primer; ss.
XX
OS Synthetic.
XX
PN JP11098997-A.
XX
PD 13-APR-1999.
XX
PF 30-JUL-1998; 98JP-0216310.
XX
PR 01-AUG-1997; 97JP-0208087.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-295324/25.

```
XX
PT   Preparation of interferon-gamma - using recombinant baculovirus and
PT   silkworm larvae
XX
PS   Example 1; Page 8; 12pp; Japanese.
XX
CC   This sequence represents a PCR primer for DNA encoding an
CC   interferon-gamma (IFN-gamma) protein.
CC   The invention relates to a method for the preparation of IFN-gamma by
CC   inactivation of recombinant baculovirus under acidic or alkaline
CC   conditions contained in a cultured supernatant of cultured insect cells
CC   infected with a recombinant virus with a DNA encoding for protein of
CC   IFN-gamma, or in body fluid extract of silkworm larvae infected with the
CC   baculovirus. The method allows for the mass production of IFN-gamma at
CC   low cost.
XX
SQ   Sequence 36 BP; 8 A; 8 C; 10 G; 10 T; 0 other;


  Query Match            72.0%;  Score 14.4;  DB 20;  Length 36;
  Best Local Similarity  93.8%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 caagcttggcaagttc 20
          || |||||||||||||
Db     31 CATGCTTGGCAAGTTC 16


RESULT   7
AAX16122/c
ID   AAX16122 standard; DNA; 36 BP.
XX
AC   AAX16122;
XX
DT   25-MAY-1999  (first entry)
XX
DE   PCR primer used in the course of the invention.
XX
KW   Protein stabilization; arabic acid; storage stability; cytokine;
KW   injectable drug composition; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9906429-A1.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-JP03431.
XX
PR   25-DEC-1997;   97JP-0357872.
PR   01-AUG-1997;   97JP-0208085.
PR   01-AUG-1997;   97JP-0208086.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Hara N,  Ito T,  Okano F,  Satoh M,  Watanabe M,  Yamada K;
PI   Yanai A;
XX
DR   WPI; 1999-153694/13.
XX
PT   Stabilisation of proteins, e.g. cytokines - by mixing with aqueous
PT   solution of arabic acid-type compound to give useful protein
PT   composition
XX
PS   Example 1; Page 64; 78pp; Japanese.
XX
CC   The present PCR primer was used in the course of the invention. The
CC   specification describes a method for the stabilizing proteins. The
CC   method comprises mixing the protein with an aqueous solution of a
CC   compound having a basic structure of arabic acid. The method is used
CC   to provide storage stability of proteins such as cytokines, e.g. as
CC   injectable drug compositions.
XX
SQ   Sequence 36 BP; 8 A; 8 C; 10 G; 10 T; 0 other;


  Query Match            72.0%;  Score 14.4;  DB 20;  Length 36;
  Best Local Similarity  93.8%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 caagcttggcaagttc 20
          || |||||||||||||
Db     31 CATGCTTGGCAAGTTC 16


RESULT   8
AAF25939/c
ID   AAF25939 standard; DNA; 36 BP.
XX
AC   AAF25939;
XX
DT   19-APR-2001  (first entry)
XX
DE   Canine gamma interferon primer SEQ ID NO 9.
XX
KW   Canine; gamma interferon; IFN-gamma; mutant; dog; antiinflammatory;
KW   silkworm nuclear polyhederosis virus; intractable canine dermatitis;
KW   primer; ss.
XX
OS   Canis sp.
XX
PN   JP2000316585-A.
XX
PD   21-NOV-2000.
XX
PF   09-JUN-1999;   99JP-0162320.
XX
PR   09-JUN-1998;   98JP-0160627.
PR   08-MAR-1999;   99JP-0059604.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-184972/19.
XX
PT   New canine interferon-gamma mutant, useful for treating intractable
PT   canine dermatitis -
XX
PS   Example 1; Page 13; 26pp; Japanese.
XX
CC   This invention describes a novel canine interferon-gamma mutant (I). The
CC   invention also describes (1) a gene (II) encoding (I); (2) preparation of
CC   (I) in which the sugar chain-combined site is removed; (3) preparation
CC   (M1) of (I) in which a recombinant silkworm nuclear polyhederosis virus
CC   gene recombined by (I) is grown in a silkworm established cell or a
CC   silkworm living body; and (4) an agent for treating intractable canine
CC   dermatitis containing (I) prepared by M1. The products of the invention
CC   have dermatological and antiinflammatory activity.
XX
SQ   Sequence 36 BP; 8 A; 8 C; 10 G; 10 T; 0 other;


  Query Match            72.0%;  Score 14.4;  DB 22;  Length 36;
  Best Local Similarity  93.8%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 caagcttggcaagttc 20
          || |||||||||||||
Db     31 CATGCTTGGCAAGTTC 16


RESULT   9
AAV39953
ID   AAV39953 standard; DNA; 33 BP.
XX
AC   AAV39953;
XX
```

DT 02-OCT-1998 (first entry)
XX
DE Streptococcus pneumoniae ORF cloning primer SEQ ID NO:436.
XX
KW Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
KW detection; pneumonia; otitis media; meningitis; cloning primer; ss.
XX
OS Synthetic.
OS Streptococcus pneumoniae.
XX
PN WO9818930-A2.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US19422.
XX
PR 31-OCT-1996; 96US-0029960.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Choi GH, Hromockyj A, Johnson LS, Kunsch CA;
XX
DR WPI; 1998-272224/24.
XX
PT Nucleic acid encoding antigenic peptide(s) from Streptococcus
PT pneumoniae - or their epitope-containing fragments, useful in
PT protective or therapeutic vaccines, and for diagnosis
XX
PS Example 1; Page 109; 118pp; English.
XX
CC The present sequence represents a cloning primer used in an example from
CC the present invention which describes proteins from Streptococcus
CC pneumoniae. Nucleic acid sequence encoding Streptococcus pneumoniae
CC proteins can be useful in vaccines for inducing protective antibodies
CC against Streptococcus pneumoniae, for treatment or prevention of
CC infection e.g. pneumonia, otitis media or meningitis. Probes based on
CC the nucleic acids are used to detect Streptococcus infection (by usual
CC hybridisation or amplification methods), also for isolating
CC Streptococcus genes or their allelic variants. The proteins can be used
CC similarly to detect specific antibodies in standard immunoassays,
CC especially for diagnosing or monitoring infections. Antibodies which
CC bind the proteins are used to detect corresponding antigens, to purify
CC the proteins and for passive immunisation (optionally coupled to a
CC toxin). Vaccines are administered, e.g. by injection, orally or through
CC the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
CC The cloning primers used in the present invention are given in AAV27437
CC to AAV27562 and AAV39870 to AAV39969.
XX
SQ Sequence 33 BP; 9 A; 7 C; 6 G; 11 T; 0 other;

Query Match 71.0%; Score 14.2; DB 19; Length 33;
Best Local Similarity 84.2%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 gaccaagcttggcaagttc 20
||| ||||||||| | |||
Db 1 gactaagcttggctaattc 19

RESULT 10
AAF80319
ID AAF80319 standard; DNA; 21 BP.
XX
AC AAF80319;
XX
DT 29-JUN-2001 (first entry)
XX
DE PCR primer used to construct plasmid pMRT1201.
XX
KW Vector; transgenesis; trfA locus; RK2 ori; oriV; P285 protein;
KW P382 protein; antibiotic resistance gene; nptIII; transgenic plant;
KW PCR primer; ss.
XX
OS Synthetic.
XX
PN FR2798139-A1.
XX
PD 09-MAR-2001.
XX
PF 03-SEP-1999; 99FR-0011112.
XX
PR 03-SEP-1999; 99FR-0011112.
XX
PA (MERI-) MERISTEM THERAPEUTICS SA.
XX
PI Gruber V, Comeau D;
XX
DR WPI; 2001-259847/27.
XX
PT New vector free from non-essential elements, useful for transforming
PT cells for protein production and for preparing transgenic plants -
XX
PS Example 1; Page 38; 180pp; French.
XX
CC The specification describes a synthetic vector containing only those
CC elements essential for its functionality and transgenesis of a cell
CC (especially a plant cell). The vector consists of at most one origin
CC of replication (ori), at most one sequence encoding a selection agent
CC and a trfA locus encoding a protein that increases the level of plasmid
CC replication. The vector particularly contains an RK2 ori, especially
CC oriV from pRK2 of Escherichia coli with a broad host range, an
CC antibiotic resistance gene (especially nptIII conferring resistance to
CC kanamycin in bacteria) and a trfA locus from pRK2 encoding the proteins
CC P285 and P382. The vectors are used to prepare transgenic plants and
CC transformed host cells for production of a heterologous proteins,
CC e.g. insulin, interferon, lipase, blood proteins and anti-inflammatory
CC agents. PCR primers AAF80318-19 were used to construct a plasmid of
CC the invention.
XX
SQ Sequence 21 BP; 5 A; 7 C; 4 G; 5 T; 0 other;

Query Match 69.0%; Score 13.8; DB 22; Length 21;
Best Local Similarity 88.2%; Pred. No. 8.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ccaagcttggcaagttc 20
||||||||||||| | |
Db 5 ccaagcttggcaattcc 21

RESULT 11
AAV42325
ID AAV42325 standard; DNA; 23 BP.
XX
AC AAV42325;
XX
DT 09-NOV-1998 (first entry)
XX
DE Basidiomycete phytase PCR primer 537.
XX
KW Phytase; basidiomycetes; feed additive; feedstuff; ss.
XX
OS Synthetic.
OS Class - Basidiomycetes.
XX
PN WO9828409-A1.
XX
PD 02-JUL-1998.
XX
PF 15-DEC-1997; 97WO-DK00568.
XX
PR 01-DEC-1997; 97DK-0001388.
PR 20-DEC-1996; 96DK-0001480.
PR 20-DEC-1996; 96DK-0001481.

```
PR   18-MAR-1997;   97DK-0000301.
PR   07-MAY-1997;   97DK-0000529.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Bech L,  Breinholt J,  Fuglsang CC,  Lassen SF,  Ohmann A;
XX
DR   WPI; 1998-377641/32.
XX
PT   Phytase(s) from fungi of phylum Basidiomycota - useful as feed and
PT   food additives, e.g. to reduce phosphate content of manure and to
PT   improve digestibility
XX
PS   Claim 7; Page 143; 197pp; English.
XX
CC   Sense primer 537 corresponds to the amino acid sequence of a
CC   conserved region (see AAW62853) of novel basidiomycete phytases
CC   (see AAW42330-35) of the invention.  It is used, preferably with
CC   antisense primer 525 (see AAV42327), in a claimed method of
CC   identifying phytase-producing cells.  The invention provides
CC   novel basidiomycete phytases, cloned DNA sequences (see
CC   AAV42330-35), processes for preparing the phytases, and their use
CC   especially as food or feed additives.
XX
SQ   Sequence 23 BP; 6 A; 5 C; 4 G; 3 T; 5 other;


  Query Match             69.0%;  Score 13.8;  DB 19;  Length 23;
  Best Local Similarity   70.6%;  Pred. No. 8.6e+02;
  Matches   12;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 ccaagcttggcaagttc 20
          |||||||||  :||:|::
Db      2 ccaagcttgayaartwy 18


RESULT  12
AAD02795
ID   AAD02795 standard; DNA; 33 BP.
XX
AC   AAD02795;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Candida albicans ERG8 coding sequence amplifying primer #1.
XX
KW   Phosphomevalonate kinase; PMK; ERG8; anti-fungal agent; diagnosis;
KW   infection; PCR primer; ss.
XX
OS   Candida albicans.
XX
PN   WO200114533-A2.
XX
PD   01-MAR-2001.
XX
PF   15-AUG-2000; 2000WO-GB03100.
XX
PR   21-AUG-1999;   99GB-0019766.
XX
PA   (ASTR ) ASTRAZENECA AB.
PA   (ASTR ) ASTRAZENECA UK LTD.
XX
PI   Rosamond JDC,  Schnell NF;
XX
DR   WPI; 2001-218441/22.
XX
PT   New polypeptides and polynucleotides (ERG8) from Candida albicans,
PT   useful in assays for identifying inhibitors of phosphomevalonate kinase
PT   activity and as reagents for diagnosing C. albicans infection  -
XX
PS   Example 4; Page 29; 29pp; English.
XX
CC   The patent discloses phosphomevalonate kinase (PMK; ERG8) protein
CC   and their corresponding DNAs from Candida albicans. The ERG8 protein
CC   is useful in assays for identifying compounds that inhibit phospho-
CC   mevalonate kinase (PMK) activity. These inhibitors are useful as
CC   anti-fungal agents. The ERG8 DNA and protein are also useful as
CC   reagents for diagnosing C. albicans infection.
CC   The present DNA sequence is PCR primer which is used to amplify the
CC   Candida albicans ERG8 coding sequence. This sequence incorporates
CC   restriction enzyme sites in the ERG8 coding sequence and facilitate
CC   its cloning.
XX
SQ   Sequence 33 BP; 10 A; 8 C; 7 G; 8 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 22;  Length 33;
  Best Local Similarity   88.2%;  Pred. No. 8.9e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 ccaagcttggcaagttc 20
          |||||||||||||  ||
Db      2 ccaagcttggcaatgtc 18


RESULT  13
AAT61665
ID   AAT61665 standard; DNA; 40 BP.
XX
AC   AAT61665;
XX
DT   18-NOV-1997  (first entry)
XX
DE   Antibody expression vector MCO5 fragment extension primer MC49.
XX
KW   Phage display vector; binding protein; Cre recombinase; antibody;
KW   polymerase chain reaction; combinatorial library; ss.
XX
OS   Synthetic.
XX
PN   WO9709436-A1.
XX
PD   13-MAR-1997.
XX
PF   05-SEP-1996;   96WO-AU00555.
XX
PR   05-SEP-1995;   95AU-0005239.
XX
PA   (CRCB-) CRC BIOPHARMACEUTICAL RES PTY LTD.
XX
PI   Hawkins NJ,  Vancov T,  Ward RL,  Zahra D;
XX
DR   WPI; 1997-192911/17.
XX
PT   Producing a phage display vector expressing both chains of a binding
PT   protein - involves site-specific recombination between a vector
PT   encoding one polypeptide chain and a vector encoding the other chain
PT   and Cre recombinase
XX
PS   Examples; Page 17; 41pp; English.
XX
CC   A new method has been developed for producing a phage display vector
CC   (PDV). The method involves recombining: (a) a vector including a
CC   sequence encoding a polypeptide chain of a specific binding pair member
CC   and (b) a phage vector including a sequence encoding Cre recombinase
CC   operatively linked to a control sequence allowing its expression; and a
CC   sequence encoding a second polypeptide chain of a specific binding pair
CC   member, in which one of the polypeptide chains is fused to and displayed
CC   at the surface of a component of a replicable genetic display package,
CC   where recombination produces a PDV including sequences encoding both
CC   polypeptide chains and where Cre recombinase expression is substantially
CC   inhibited. The present sequence represents a primer MC49 used to extend
CC   the ends of the antibody expression vector fragment MCO5, for use in the
CC   construction of Term-LacVH cassette. Antibodies displayed on the PDV
CC   surface can have a desired antigen specificity. The PDV are suitable for
CC   preparing combinatorial libraries of antibodies. Stable recombinants are
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CC   produced, compared with prior art in which the recombination process is
CC   reversible. The inclusion of a selectable marker allows easier selection
CC   of recombinants and large antibody libraries can be generated.
XX
SQ   Sequence 40 BP; 13 A; 9 C; 6 G; 12 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 18;  Length 40;
  Best Local Similarity   88.2%;  Pred. No. 9.1e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 ccaagcttggcaagttc 20
           |||||||||| ||| ||
Db       2 ccaagcttgggaagatc 18


RESULT  14
AAQ42332/c
ID   AAQ42332 standard; DNA; 54 BP.
XX
AC   AAQ42332;
XX
DT   08-SEP-1993  (first entry)
XX
DE   Gamma globin gene primer GAM-3-H.
XX
KW   Embryonic; zeta; epsilon; fetal; gamma; adult; delta; alpha; beta;
KW   haemoglobin; methionine aminopeptidase; oxygen affinity; HbF Chico;
KW   post-translational modification; HbA Deer Lodge; HbA Abruzzo; yeast;
KW   Hb Portland Titusville; HbA Motown/Hacettepe; alkaline stablility;
KW   HbA McKees Rock; transformation; Hb BovII; blood substitute solution;
KW   globin; physiological; oxygen carrier; plasma expander; primer; PCR;
KW   polymerase chain reaction; amplify; YEp51T/G; expression vector; ss.
XX
OS   Synthetic.
XX
PN   WO9308831-A.
XX
PD   13-MAY-1993.
XX
PF   30-OCT-1991;   91WO-US08108.
XX
PR   30-OCT-1991;   91WO-US08108.
XX
PA   (STRO-) STROHTECH INC.
XX
PI   Bajwa W,  De Angelo J,  Motwani NM;
XX
DR   WPI; 1993-167394/20.
XX
PT   New haemoglobin variants bind reversibly to oxygen - useful as
PT   physiological oxygen carriers (e.g. in blood substitutes) and as
PT   plasma expanders
XX
PS   Disclosure; Fig 14B; 211pp; English.
XX
CC   The sequences given in AAQ42331-32 are primers which were used in the
CC   isolation of the gamma globin gene (see also AAQ42330).  The plasmid
CC   pJW151 was used as a template.  The amplified DNA sequence was
CC   cloned into the plasmid YEp51T/NAT which had the beta globin gene
CC   removed, to produce a yeast expression vector, YEp51T/G, which was
CC    used to transform E. coli DH5-alpha cells.  A mutation in the codon
CC   representing Lys66 causing it to encode Thr produces the low oxygen
CC   globin varient, HbF Chico (see also AAR39721).  The varient gamma
CC   globin may be used in applications which require physiological
CC   oxygen carriers, such as in blood substitute solutions, or as
CC   plasma expanders.
XX
SQ   Sequence 54 BP; 10 A; 14 C; 19 G; 11 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 14;  Length 54;
  Best Local Similarity   93.3%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 tgaccaagcttggca 15
           ||||||||||| |||
Db      21 TGACCAAGCTTAGCA 7


RESULT  15
AAV08758/c
ID   AAV08758 standard; DNA; 54 BP.
XX
AC   AAV08758;
XX
DT   18-FEB-1999  (first entry)
XX
DE   PCR primer GAM-3-H for human haemoglobin mutant.
XX
KW   Haemoglobin; mutant; human; substitute blood product; synthetic blood;
KW   beta chain; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5827693-A.
XX
PD   27-OCT-1998.
XX
PF   07-JUN-1995;   95US-0484686.
XX
PR   29-APR-1992;   92US-0876290.
PR   16-APR-1990;   90US-0509918.
PR   14-NOV-1990;   90US-0614359.
PR   12-APR-1991;   91US-0684611.
PR   29-DEC-1994;   94US-0368407.
PR   07-JUN-1995;   95US-0484686.
XX
PA   (APEX-) APEX BIOSCIENCE INC.
XX
PI   Bajwa W,  Bonaventura J,  De Angelo J,  Motwani NM;
XX
DR   WPI; 1998-593993/50.
XX
PT   Recombinant expression of globin chains - and variants in yeast,
PT   useful as substitutes for natural blood required for oxygen carriage
XX
PS   Example 3; Fig 14; 144pp; English.
XX
CC   This sequence represents a PCR primer for DNA encoding a human
CC   haemoglobin variant. The amplified DNA is used in the recombinant DNA
CC   vector of the invention, which expresses a globin chain in a yeast cell,
CC   and comprises: (a) a first DNA sequence encoding a globin chain; (b) a
CC   yeast transcriptional promoter which promotes the transcription of the
CC   first DNA sequence; (c) a second DNA sequence encoding a yeast selectable
CC   marker; and (d) a yeast replication origin. The vectors and recombinant
CC   yeast cells containing them can be used for the recombinant production of
CC   the globin chains and their variants. The products in turn, can be used
CC   as substitute blood products, where oxygen carriage is required. The
CC   variants are designed to enable generally stable cross-linking of
CC   monomers to a tetrameric form, which does not dissociate into dimers.
CC   They are also designed to be stable to a certain extent in alkaline
CC   conditions compared to normal physiological conditions. The yeast strains
CC   used allow recombinant production of correctly processed haemoglobin
CC   chains in large quantities. The use of recombinant blood also eliminates
CC   risks of contamination of donated blood samples, and also shortages of
CC   not having enough donations of a specific blood type.
CC   N.B. This sequence was created from the human haemoglobin beta chain
CC   sequence given in the specification.
XX
SQ   Sequence 54 BP; 10 A; 14 C; 19 G; 11 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 19;  Length 54;
  Best Local Similarity   93.3%;  Pred. No. 1.5e+03;
```

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 tgaccaagcttggca 15
           ||||||||||| |||
Db      21 TGACCAAGCTTAGCA 7
```

Search completed: March 13, 2002, 09:50:42
Job time: 5151 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 09:50:30 ; Search time 1263.07 Seconds
(without alignments)
13.575 Million cell updates/sec

Title: US-09-923-515-16
Perfect score: 20
Sequence: 1 tgaccaagcttggcaggttc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

earched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:*
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21: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	26	20	AAX89305	Primer used in RT-
2	14.2	71.0	49	21	AAC99322	Human serum albumi
3	14.2	71.0	49	21	AAC99469	Human serum albumi
c 4	14.2	71.0	50	21	AAC99321	Human serum albumi
c 5	14.2	71.0	50	21	AAC99468	Human serum albumi
c 6	13.8	69.0	20	20	AAZ31293	CCR5 gene inhibiti
7	13.8	69.0	33	21	AAA11151	Primer 6456 for hu
8	13.8	69.0	33	21	AAA12609	PCR primer 6456 us
9	13.8	69.0	44	22	AAF56975	FIV gene cloning f
10	13.4	67.0	24	19	AAV43309	PCR primer used to
c 11	13.4	67.0	34	18	AAT60277	IGF-BP3 gene p53-b
12	13.4	67.0	34	18	AAT60279	IGF-BP3 gene p53-b
c 13	13.4	67.0	54	14	AAQ42332	Gamma globin gene
c 14	13.4	67.0	54	19	AAV08758	PCR primer GAM-3-H
c 15	13.4	67.0	54	22	AAF31402	Oligonucleotide.
16	13.2	66.0	24	21	AAA38088	Oligonucleotide OD
17	13.2	66.0	24	21	AAA14544	Primer ODN-RT(-) w
18	13.2	66.0	24	21	AAA14553	Oligonucleotide 3'
19	13.2	66.0	24	22	AAS02282	Moloney murine leu
20	13.2	66.0	24	22	AAS02674	Oligodeoxynucleoti
c 21	13	65.0	15	17	AAT37558	Apo(a) mRNA (nt. p
22	12.8	64.0	21	15	AAQ78742	Murine anti-human
23	12.8	64.0	21	19	AAV53747	Nucleotide sequenc
c 24	12.8	64.0	36	20	AAX36413	PCR primer for IFN
c 25	12.8	64.0	36	20	AAX16122	PCR primer used in
c 26	12.8	64.0	36	22	AAF25939	Canine gamma inter
27	12.8	64.0	42	21	AAZ88412	H. pylori antigen
28	12.8	64.0	57	17	AAT12257	Cytochrome P450 CY
c 29	12.6	63.0	22	21	AAA27233	Reverse PCR primer
c 30	12.6	63.0	22	21	AAA30354	FGFR3 mRNA PCR pri
31	12.6	63.0	25	20	AAX88714	Detector oligonucl
32	12.6	63.0	25	21	AAA60951	Detector oligonucl
33	12.6	63.0	25	21	AAA57470	Detector oligonucl
34	12.6	63.0	25	22	AAF31212	High throughput as
35	12.6	63.0	28	8	AAN70798	DNA encoding mutan
36	12.6	63.0	33	19	AAV39953	Streptococcus pneu
c 37	12.6	63.0	35	21	AAC64260	Soybean cotyledon
c 38	12.6	63.0	60	20	AAX88713	RNA mimic oligonuc
c 39	12.6	63.0	60	21	AAA60950	Mouse GAPDH RNA mi
c 40	12.6	63.0	60	21	AAA57469	Mimic of the murin
41	12.4	62.0	20	21	AAA98818	HPV18 specific pri
42	12.4	62.0	20	22	AAH42683	Primer and probe f
43	12.4	62.0	25	21	AAZ97493	HIV-1 protease gen
c 44	12.4	62.0	26	13	AAQ25288	PCR primer for Hin
c 45	12.4	62.0	26	13	AAQ31240	Factor IX targetti

ALIGNMENTS

RESULT 1
AAX89305
ID AAX89305 standard; DNA; 26 BP.
XX
AC AAX89305;
XX
DT 21-SEP-1999 (first entry)
XX
DE Primer used in RT-PCR analysis of transgenic apo(a).
XX
KW Transgenic rabbit; apolipoprotein (a); apolipoprotein B; lipoprotein;
KW atherosclerotic lesion; cholesterol; vascular injury; restenosis; apoB;
KW RT-PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9935241-A1.
XX
PD 15-JUL-1999.
XX
PF 08-JAN-1999; 99WO-US00401.
XX
PR 08-JAN-1998; 98US-0070727.
XX
PA (RHON) RHONE-POULENC RORER PHARM INC.
XX
PI Denefle P, Duverger N, Emmanuel F, Houdebine L;
PI Hughes SD, Rouy D, Rubin E, Viglietta C;
XX
DR WPI; 1999-430386/36.
XX
PT A transgenic rabbit that expresses a functional human lipoprotein A
XX
PS Example 3; Page 46; 73pp; English.

```
XX
CC   The invention provides a transgenic rabbit, which has in its genomic
CC   DNA, sequences that encode apolipoprotein (a) and apolipoprotein B
CC   polypeptides, which are capable of combining to produce lipoprotein (a).
CC   The transgenic rabbit expresses a functional human lipoprotein (a). The
CC   rabbit develops human-like atherosclerotic lesions when fed a
CC   cholesterol rich diet. The transgenic rabbit is useful as a model for
CC   human diseases that are induced and/or exacerbated by lipoprotein (a)
CC   expression. The model can be used to identify inhibitors of lipoprotein
CC   (a) particle assembly and inhibitors of lipoprotein (a) associated
CC   diseases. The rabbit model is advantageous, when compared to the mouse,
CC   due partly to its relatively larger size, enabling facile studies of
CC   vascular injury and restenosis. In addition, while rabbits are similar to
CC   mice in lacking apo(a) and lipoprotein (a), their lipoprotein profile
CC   more closely mimics that of humans, with LDL as the predominant plasma
CC   lipoprotein. Sequences AAX89305-308 represent priomers used in the
CC   analysisi of transgenic apo(a) and apoB.
XX
SQ   Sequence 26 BP; 5 A; 7 C; 7 G; 7 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 20;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.9;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tgaccaagcttggcaggttc 20
          ||||||||||||||||||||
Db      3 tgaccaagcttggcaggttc 22


RESULT   2
AAC99322
ID   AAC99322 standard; DNA; 49 BP.
XX
AC   AAC99322;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human serum albumin (HSA) related oligonucleotide A-9.
XX
KW   Human serum albumin; HSA; ss.
XX
OS   Homo sapiens.
XX
PN   CN1266099-A.
XX
PD   13-SEP-2000.
XX
PF   04-MAR-1999;   99CN-0102745.
XX
PR   04-MAR-1999;   99CN-0102745.
XX
PA   (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI   Liu Z;
XX
DR   WPI; 2000-673206/66.
XX
PT   Novel methods for chemical synthesis, expression and recombinant
PT   protein production for human serum albumin reformed gene -
XX
PS   Example 2; Fig 8; 85pp; Chinese.
XX
CC   The present invention relates to two kinds of DNA sequences of coded
CC   human serum albumin (HSA), i.e. design of structure-modified gene
CC   segment of HSA and artificial total synthesis and a production process
CC   for large-scale production of genetic recombinant HSA by using
CC   methanol, yeast and engineering bacterium, and discovers that the
CC   structure-modified gene can greatly increase the expression quantity
CC   of HSA. The production process can make the structural gene of HSA
CC   obtain high-level expression under the drive of promoter induced by
CC   methanol, and make the HSA expression product secrete into the
CC   fermenting liquor culture medium, and provide reliable test data for
CC   more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC   to AAC99391 represent oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 49 BP; 7 A; 11 C; 12 G; 19 T; 0 other;


  Query Match             71.0%;  Score 14.2;  DB 21;  Length 49;
  Best Local Similarity   84.2%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 tgaccaagcttggcaggtt 19
          | ||||| ||||||| |||
Db     14 taaccaatcttggcaagtt 32


RESULT   3
AAC99469
ID   AAC99469 standard; DNA; 49 BP.
XX
AC   AAC99469;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human serum albumin (HSA) related oligonucleotide A-9.
XX
KW   Human serum albumin; HSA; ss.
XX
OS   Homo sapiens.
XX
PN   CN1266100-A.
XX
PD   13-SEP-2000.
XX
PF   04-MAR-1999;   99CN-0102794.
XX
PR   04-MAR-1999;   99CN-0102794.
XX
PA   (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI   Liu Z;
XX
DR   WPI; 2000-673207/66.
XX
PT   Novel methods for the chemical synthesis, expression and recombinant
PT   protein production for human serum albumin reformed gene -
XX
PS   Example 2; Fig 8; 85pp; Chinese.
XX
CC   The present invention relates to two kinds of DNA sequences of coded
CC   human serum albumin (HSA), i.e. design of structure-modified gene
CC   segment of HSA and artificial total synthesis and a production process
CC   for large-scale production of genetic recombinant HSA by using
CC   methanol, yeast and engineering bacterium, and discovers that the
CC   structure-modified gene can greatly increase the expression quantity
CC   of HSA. The production process can make the structural gene of HSA
CC   obtain high-level expression under the drive of promoter induced by
CC   methanol, and make the HSA expression product secrete into the
CC   fermenting liquor culture medium, and provide reliable test data for
CC   more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC   to AAC99391 represent oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 49 BP; 7 A; 11 C; 12 G; 19 T; 0 other;


  Query Match             71.0%;  Score 14.2;  DB 21;  Length 49;
  Best Local Similarity   84.2%;  Pred. No. 6.5e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 tgaccaagcttggcaggtt 19
          | ||||| ||||||| |||
Db     14 taaccaatcttggcaagtt 32
```

RESULT 4
AAC99321/c
ID AAC99321 standard; DNA; 50 BP.
XX
AC AAC99321;
XX
DT 07-MAR-2001 (first entry)
XX
DE Human serum albumin (HSA) related oligonucleotide A-8.
XX
KW Human serum albumin; HSA; ss.
XX
OS Homo sapiens.
XX
PN CN1266099-A.
XX
PD 13-SEP-2000.
XX
PF 04-MAR-1999; 99CN-0102745.
XX
PR 04-MAR-1999; 99CN-0102745.
XX
PA (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI Liu Z;
XX
DR WPI; 2000-673206/66.
XX
PT Novel methods for chemical synthesis, expression and recombinant
PT protein production for human serum albumin reformed gene -
XX
PS Example 2; Fig 8; 85pp; Chinese.
XX
CC The present invention relates to two kinds of DNA sequences of coded
CC human serum albumin (HSA), i.e. design of structure-modified gene
CC segment of HSA and artificial total synthesis and a production process
CC for large-scale production of genetic recombinant HSA by using
CC methanol, yeast and engineering bacterium, and discovers that the
CC structure-modified gene can greatly increase the expression quantity
CC of HSA. The production process can make the structural gene of HSA
CC obtain high-level expression under the drive of promoter induced by
CC methanol, and make the HSA expression product secrete into the
CC fermenting liquor culture medium, and provide reliable test data for
CC more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC to AAC99391 represent oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 50 BP; 20 A; 13 C; 11 G; 6 T; 0 other;

Query Match 71.0%; Score 14.2; DB 21; Length 50;
Best Local Similarity 84.2%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccaagcttggcaggtt 19
| ||||| ||||||| |||
Db 41 TAACCAATCTTGGCAAGTT 23

RESULT 5
AAC99468/c
ID AAC99468 standard; DNA; 50 BP.
XX
AC AAC99468;
XX
DT 07-MAR-2001 (first entry)
XX
DE Human serum albumin (HSA) related oligonucleotide A-8.
XX
KW Human serum albumin; HSA; ss.
XX
OS Homo sapiens.
XX
PN CN1266100-A.
XX
PD 13-SEP-2000.
XX
PF 04-MAR-1999; 99CN-0102794.
XX
PR 04-MAR-1999; 99CN-0102794.
XX
PA (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI Liu Z;
XX
DR WPI; 2000-673207/66.
XX
PT Novel methods for the chemical synthesis, expression and recombinant
PT protein production for human serum albumin reformed gene -
XX
PS Example 2; Fig 8; 85pp; Chinese.
XX
CC The present invention relates to two kinds of DNA sequences of coded
CC human serum albumin (HSA), i.e. design of structure-modified gene
CC segment of HSA and artificial total synthesis and a production process
CC for large-scale production of genetic recombinant HSA by using
CC methanol, yeast and engineering bacterium, and discovers that the
CC structure-modified gene can greatly increase the expression quantity
CC of HSA. The production process can make the structural gene of HSA
CC obtain high-level expression under the drive of promoter induced by
CC methanol, and make the HSA expression product secrete into the
CC fermenting liquor culture medium, and provide reliable test data for
CC more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC to AAC99391 represent oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 50 BP; 20 A; 13 C; 11 G; 6 T; 0 other;

Query Match 71.0%; Score 14.2; DB 21; Length 50;
Best Local Similarity 84.2%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 tgaccaagcttggcaggtt 19
| ||||| ||||||| |||
Db 41 TAACCAATCTTGGCAAGTT 23

RESULT 6
AAZ31293/c
ID AAZ31293 standard; DNA; 20 BP.
XX
AC AAZ31293;
XX
DT 24-JAN-2000 (first entry)
XX
DE CCR5 gene inhibiting antisense oligo AS(s)-50.
XX
KW HIV cofactor inhibitor; HIV infection; CXCR4 gene; CCR5 gene;
KW drug composition; antisense; ss.
XX
OS Synthetic.
XX
PN WO9951751-A1.
XX
PD 14-OCT-1999.
XX
PF 01-APR-1999; 99WO-JP01722.
XX
PR 02-APR-1998; 98JP-0125452.
XX
PA (MARI-) MARINE BIO CO LTD.
XX
PI Takaku H, Yamamoto N, Kimura T, Takai K, Wada A;

XX
DR WPI; 1999-620207/53.
XX
PT Antisense oligonucleotide-based HIV cofactor inhibitors, as drug
PT compositions for treatment of HIV infection -
XX
PS Claim 6; Page 16; 59pp; Japanese.
XX
CC The invention provides HIV cofactor inhibitors that contain
CC oligonucleotides with a base sequence complementary to the CXCR4 or CCR5
CC genes. Such inhibitors can be formulated into drug compositions for
CC prevention or treatment of HIV infection, with inhibition of expression
CC of CXCR4 or/and CCR5 gene. Sequences AAZ31244-306 represent antisense
CC oligonucleotides to the CCR5 gene.
XX
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 other;

Query Match 69.0%; Score 13.8; DB 20; Length 20;
Best Local Similarity 88.2%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 gaccaagcttggcaggt 18
||||||||| ||||||
Db 19 GACCAAGCTATGCAGGT 3

RESULT 7
AAA11151
ID AAA11151 standard; DNA; 33 BP.
XX
AC AAA11151;
XX
DT 11-OCT-2000 (first entry)
XX
DE Primer 6456 for human smooth muscle cell alpha-actin gene promoter.
XX
KW Hybrid promoter; enhancer region; ubiquitous promoter; PCR primer;
KW smooth-muscle cell; alpha-actin; expression cassette; vector; mutant;
KW endothelial cell; blood vessel; transgenic animal; gene therapy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN FR2783839-A1.
XX
PD 31-MAR-2000.
XX
PF 25-SEP-1998; 98FR-0012000.
XX
PR 25-SEP-1998; 98FR-0012000.
XX
PA (RHON) RHONE-POULENC RORER SA.
XX
PI Branellec D, Darteil R, Mahfoudi A, Scherman D;
XX
DR WPI; 2000-285251/25.
XX
PT Hybrid promoter useful for gene expression in smooth-muscle cells
PT includes the enhancer region of a ubiquitous strong promoter/enhancer
PT -
XX
PS Example 1; Page 18; 47pp; French.
XX
CC The invention relates to the generation of new hybrid promoters
CC comprising: (a) at least part of the enhancer region of a ubiquitous
CC strong promoter/enhancer; and (b) a promoter region permitting specific
CC expression in smooth-muscle cells. The primers AAA11150-A11151 were used
CC to PCR amplify the promoter region of the human smooth muscle cell
CC alpha-actin gene and to introduce an XhoI restriction enzyme site.
CC The hybrid promoter is useful for preparing expression cassettes and
CC vectors for tissue-specific expression of RNA or polypeptide molecules
CC of interest in smooth-muscle cells, especially in the absence of
CC expression in endothelial cells in the vicinity of blood vessels, e.g.
CC for the purpose of producing recombinant proteins, for creating
CC transgenic animal models or cell lines, for performing screening
CC assays or for gene therapy.
XX
SQ Sequence 33 BP; 5 A; 11 C; 10 G; 7 T; 0 other;

Query Match 69.0%; Score 13.8; DB 21; Length 33;
Best Local Similarity 88.2%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 tgaccaagcttggcagg 17
|||| ||||||||| ||
Db 4 tgacaaagcttggctgg 20

RESULT 8
AAA12609
ID AAA12609 standard; DNA; 33 BP.
XX
AC AAA12609;
XX
DT 25-JUL-2000 (first entry)
XX
DE PCR primer 6456 used to amplify the promoter of alpha-actin gene.
XX
KW Smooth muscle alpha-actin gene promoter; hybrid promoter; gene therapy;
KW enhancer region; enhancer; smooth-muscle cell; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200018908-A1.
XX
PD 06-APR-2000.
XX
PF 23-SEP-1999; 99WO-FR02265.
XX
PR 25-SEP-1998; 98FR-0012000.
PR 04-MAR-1999; 99US-0123298.
XX
PA (AVET) AVENTIS PHARMA SA.
XX
PI Branellec D, Darteil R, Mahfoudi A, Scherman D;
XX
DR WPI; 2000-293147/25.
XX
PT Hybrid promoter useful for gene expression in smooth-muscle cells
PT includes the enhancer region of a ubiquitous strong promoter/enhancer
PT -
XX
PS Example 1; Page 18; 51pp; French.
XX
CC PCR primers AAA12608-09 were used to amplify the promoter of human
CC smooth muscle alpha-actin gene, and to introduce restriction sites into
CC the sequence. The amplified fragment is used to construct the hybrid
CC promoters of the invention. These hybrid promoters comprise at least
CC part of the enhancer region of a ubiquitous strong promoter/enhancer,
CC and a promoter region permitting specific expression in smooth-muscle
CC cells. The hybrid promoter is useful for preparing expression cassettes
CC and vectors for tissue-specific expression of RNA or polypeptide
CC molecules of interest in smooth-muscle cells, especially in the absence
CC of expression in endothelial cells in the vicinity of blood vessels,
CC e.g. for the purpose of producing recombinant proteins, for creating
CC transgenic animal models or cell lines, for performing screening assays
CC or for gene therapy.
XX
SQ Sequence 33 BP; 5 A; 11 C; 10 G; 7 T; 0 other;

Query Match 69.0%; Score 13.8; DB 21; Length 33;
Best Local Similarity 88.2%; Pred. No. 9.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy       1 tgaccaagcttggcagg 17
           |||| ||||||||| ||
Db       4 tgacaaagcttggctgg 20


RESULT   9
AAF56975
ID   AAF56975 standard; DNA; 44 BP.
XX
AC   AAF56975;
XX
DT   14-MAY-2001  (first entry)
XX
DE   FIV gene cloning forward primer.
XX
KW   FIV; feline immunodeficiency virus; FIV-141; vaccine; antigen; GAG; POL;
KW   polymerase; envelope; ENV; regulatory protein; immune response; cat;
KW   antiviral; PCR primer; ss.
XX
OS   Feline immunodeficiency virus.
XX
PN   EP1074625-A2.
XX
PD   07-FEB-2001.
XX
PF   09-JUN-2000; 2000EP-0304924.
XX
PR   14-JUN-1999;   99US-0138999.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Deng R,  Jeevarathnam S,  Fuog ED,  Koertje WD,  Johnson AF;
PI   Sheppard MG,  Yule TD,  Roth MB,  Wheeler DW;
XX
DR   WPI; 2001-193156/20.
XX
PT   Vaccines useful for preventing feline immunodeficiency virus (FIV)
PT   comprise a polynucleotide or a polypeptide from the genome of the
PT   FIV-141 strain, specifically FIV-141 (ATCC VR-2619) -
XX
PS   Claim 52; Page 23; 53pp; English.
XX
CC   The invention relates to a new vaccine against feline immunodeficiency
CC   virus (FIV) comprising a polynucleotide having a sequence from a portion
CC   of the genome of an FIV-141 strain, specifically FIV-141 (ATCC VR-2619)
CC   and a carrier. The vaccine against FIV comprises one or more group
CC   antigen (GAG), polymerase (POL), envelope (ENV) or regulatory protein
CC   from an FIV strain. The vaccine is used for inducing immune or protective
CC   response in cats against FIV. Unlike previous vaccines against FIV, the
CC   new vaccine is capable of inducing a protective response in a cat against
CC   homologous and heterologous challenge. Sequences AAF56959-990 represent
CC   PCR primers used for cloning FIV genes into eukaryotic expression
CC   vectors.
XX
SQ   Sequence 44 BP; 11 A; 12 C; 11 G; 10 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 22;  Length 44;
  Best Local Similarity   88.2%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tgaccaagcttggcagg 17
           |||| ||| ||||||||
Db      28 tgacgaagattggcagg 44


RESULT  10
AAV43309
ID   AAV43309 standard; DNA; 24 BP.
XX
AC   AAV43309;
XX
DT   26-OCT-1998  (first entry)
XX
DE   PCR primer used to amplify nucleic acid ligands for ICP4.
XX
KW   ICP4; transcriptional regulator; Herpes simplex virus; HSV;
KW   nucleic acid ligand; treatment; prevention; disease; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   US5795721-A.
XX
PD   18-AUG-1998.
XX
PF   25-JAN-1996;   96US-0591989.
XX
PR   25-JAN-1996;   96US-0591989.
PR   11-JUN-1990;   90US-0536428.
PR   10-JUN-1991;   91US-0714131.
PR   24-MAR-1995;   95US-0409442.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
XX
PI   Gold L,  Jayasena SD,  Rabin RS;
XX
DR   WPI; 1998-466659/40.
XX
PT   Identification of nucleic acid ligands to ICP4 protein family member
PT   - comprises preparing candidate mixture of nucleic acids, contacting
PT   candidate mixture of nucleic acids with ICP4, partitioning increased
PT   affinity nucleic acids, and amplifying
XX
PS   Example 1; Column 24; 36pp; English.
XX
CC   PCR primers AAV43309-10 were used to amplify nucleic acid ligands of
CC   ICP4, which were isolated using the SELEX (Systematic Evolution of
CC   Ligands by Exponential enrichment) procedure. ICP4 is the major
CC   transcriptional regulator of Herpes simplex virus (HSV) gene expression.
CC   The specification describes a method for the identification of nucleic
CC   acid ligands to an ICP4 protein family member (PFM), which uses the
CC   SELEX procedure. The method is used to yield a mixture of nucleic acids
CC   enriched for nucleic acid sequences with relatively higher affinity and
CC   specificity for binding ICP4 protein family member. The nucleic acid
CC   ligands identified are used in the treatment or prevention of diseases
CC   or medical conditions in humans, specifically those caused by herpes
CC   viruses. They may also be used in diagnostic procedures.
XX
SQ   Sequence 24 BP; 6 A; 5 C; 10 G; 3 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 19;  Length 24;
  Best Local Similarity   93.3%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 accaagcttggcagg 17
           |||||||||||| |||
Db       1 accaagcttgggagg 15


RESULT  11
AAT60277/c
ID   AAT60277 standard; DNA; 34 BP.
XX
AC   AAT60277;
XX
DT   26-NOV-1997  (first entry)
XX
DE   IGF-BP3 gene p53-binding element.
XX
KW   Insulin-like growth factor binding protein-3; IGF-BP3; p53;
KW   tumour suppressor; ds.
XX
OS   Homo sapiens.
XX
```

```
FH   Key             Location/Qualifiers
FT   misc_binding    10..29
FT                   /*tag= a
FT                   /note= "p53-binding element (nts 4078-4097)"
XX
PN   WO9709998-A2.
XX
PD   20-MAR-1997.
XX
PF   12-SEP-1996;   96WO-US14623.
XX
PR   14-SEP-1995;   95US-0003730.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Buckbinder L,  Kley NA,  Seizinger BR;
XX
DR   WPI; 1997-202005/18.
XX
PT   Treatment of p53-related tumours - using insulin-like growth factor
PT   binding protein-3 or a modulator of its expression or activity
XX
PS   Claim 2; Page 10; 28pp; English.
XX
CC   This DNA sequence is a p53-binding DNA element found in intron 2
CC   (nts 4079-97) of the insulin-like growth factor binding protein-3
CC   (IGF-BP3) gene.  This, and another DNA element (see AAT60276), were
CC   determined by computer analysis to have similarity to the p53
CC   consensus binding site.  Claimed methods for treating p53-related
CC   tumours comprise administering a modulator of IGF-BP3 that
CC   upregulates IGF-BP3 expression or activity, administering IGF-BP3
CC   or administering an expression vector encoding IGF-BP3.  A method
CC   of identifying a substance useful in the treatment of p53-related
CC   tumours comprises (a) applying a test substance to a cell having
CC   an expression vector containing a reporter gene linked to one or
CC   both of the p53-binding elements from the IGF-BP3 gene, and (b)
CC   analysing the cell to detect expression of the reporter gene.
XX
SQ   Sequence 34 BP; 9 A; 8 C; 13 G; 4 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 18;  Length 34;
  Best Local Similarity   93.3%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 ccaagcttggcaggt 18
           ||| ||||||||||||
Db      31 CCAGGCTTGGCAGGT 17


RESULT  12
AAT60279
ID   AAT60279 standard; DNA; 34 BP.
XX
AC   AAT60279;
XX
DT   26-NOV-1997  (first entry)
XX
DE   IGF-BP3 gene p53-binding element consensus competitor.
XX
KW   Insulin-like growth factor binding protein-3; IGF-BP3; p53;
KW   tumour suppressor; ds.
XX
OS   Synthetic.
XX
PN   WO9709998-A2.
XX
PD   20-MAR-1997.
XX
PF   12-SEP-1996;   96WO-US14623.
XX
PR   14-SEP-1995;   95US-0003730.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Buckbinder L,  Kley NA,  Seizinger BR;
XX
DR   WPI; 1997-202005/18.
XX
PT   Treatment of p53-related tumours - using insulin-like growth factor
PT   binding protein-3 or a modulator of its expression or activity
XX
PS   Disclosure; Page 10; 28pp; English.
XX
CC   A consensus competitor (AAT60279) and mutant competitor (AAT60280)
CC   were used in experiments for the characterisation of 2 p53-binding
CC   and -responsive elements (see AAT60276-77) found in the insulin-like
CC   growth factor binding protein-3 (IGF-BP3) gene.  The results
CC   demonstrated specific binding of p53 to the p53-binding elements
CC   and that the p53-binding elements confer p53-inducibility to a
CC   heterologous promoter.
XX
SQ   Sequence 34 BP; 4 A; 13 C; 8 G; 9 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 18;  Length 34;
  Best Local Similarity   93.3%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 ccaagcttggcaggt 18
           ||| ||||||||||||
Db       8 ccaggcttggcaggt 22


RESULT  13
AAQ42332/c
ID   AAQ42332 standard; DNA; 54 BP.
XX
AC   AAQ42332;
XX
DT   08-SEP-1993  (first entry)
XX
DE   Gamma globin gene primer GAM-3-H.
XX
KW   Embryonic; zeta; epsilon; fetal; gamma; adult; delta; alpha; beta;
KW   haemoglobin; methionine aminopeptidase; oxygen affinity; HbF Chico;
KW   post-translational modification; HbA Deer Lodge; HbA Abruzzo; yeast;
KW   Hb Portland Titusville; HbA Motown/Hacettepe; alkaline stablility;
KW   HbA McKees Rock; transformation; Hb BovII; blood substitute solution;
KW   globin; physiological; oxygen carrier; plasma expander; primer; PCR;
KW   polymerase chain reaction; amplify; YEp51T/G; expression vector; ss.
XX
OS   Synthetic.
XX
PN   WO9308831-A.
XX
PD   13-MAY-1993.
XX
PF   30-OCT-1991;   91WO-US08108.
XX
PR   30-OCT-1991;   91WO-US08108.
XX
PA   (STRO-) STROHTECH INC.
XX
PI   Bajwa W,  De Angelo J,  Motwani NM;
XX
DR   WPI; 1993-167394/20.
XX
PT   New haemoglobin variants bind reversibly to oxygen - useful as
PT   physiological oxygen carriers (e.g. in blood substitutes) and as
PT   plasma expanders
XX
PS   Disclosure; Fig 14B; 211pp; English.
XX
CC   The sequences given in AAQ42331-32 are primers which were used in the
CC   isolation of the gamma globin gene (see also AAQ42330).  The plasmid
```

CC pJW151 was used as a template. The amplified DNA sequence was
CC cloned into the plasmid YEp51T/NAT which had the beta globin gene
CC removed, to produce a yeast expression vector, YEp51T/G, which was
CC used to transform E. coli DH5-alpha cells. A mutation in the codon
CC representing Lys66 causing it to encode Thr produces the low oxygen
CC globin varient, HbF Chico (see also AAR39721). The varient gamma
CC globin may be used in applications which require physiological
CC oxygen carriers, such as in blood substitute solutions, or as
CC plasma expanders.
XX
SQ Sequence 54 BP; 10 A; 14 C; 19 G; 11 T; 0 other;

Query Match 67.0%; Score 13.4; DB 14; Length 54;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccaagcttggca 15
||||||||||| |||
Db 21 TGACCAAGCTTAGCA 7

RESULT 14
AAV08758/c
ID AAV08758 standard; DNA; 54 BP.
XX
AC AAV08758;
XX
DT 18-FEB-1999 (first entry)
XX
DE PCR primer GAM-3-H for human haemoglobin mutant.
XX
KW Haemoglobin; mutant; human; substitute blood product; synthetic blood;
KW beta chain; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5827693-A.
XX
PD 27-OCT-1998.
XX
PF 07-JUN-1995; 95US-0484686.
XX
PR 29-APR-1992; 92US-0876290.
PR 16-APR-1990; 90US-0509918.
PR 14-NOV-1990; 90US-0614359.
PR 12-APR-1991; 91US-0684611.
PR 29-DEC-1994; 94US-0368407.
PR 07-JUN-1995; 95US-0484686.
XX
PA (APEX-) APEX BIOSCIENCE INC.
XX
PI Bajwa W, Bonaventura J, De Angelo J, Motwani NM;
XX
DR WPI; 1998-593993/50.
XX
PT Recombinant expression of globin chains - and variants in yeast,
PT useful as substitutes for natural blood required for oxygen carriage
XX
PS Example 3; Fig 14; 144pp; English.
XX
CC This sequence represents a PCR primer for DNA encoding a human
CC haemoglobin variant. The amplified DNA is used in the recombinant DNA
CC vector of the invention, which expresses a globin chain in a yeast cell,
CC and comprises: (a) a first DNA sequence encoding a globin chain; (b) a
CC yeast transcriptional promoter which promotes the transcription of the
CC first DNA sequence; (c) a second DNA sequence encoding a yeast selectable
CC marker; and (d) a yeast replication origin. The vectors and recombinant
CC yeast cells containing them can be used for the recombinant production of
CC the globin chains and their variants. The products in turn, can be used
CC as substitute blood products, where oxygen carriage is required. The
CC variants are designed to enable generally stable cross-linking of
CC monomers to a tetrameric form, which does not dissociate into dimers.
CC They are also designed to be stable to a certain extent in alkaline
CC conditions compared to normal physiological conditions. The yeast strains
CC used allow recombinant production of correctly processed haemoglobin
CC chains in large quantities. The use of recombinant blood also eliminates
CC risks of contamination of donated blood samples, and also shortages of
CC not having enough donations of a specific blood type.
CC N.B. This sequence was created from the human haemoglobin beta chain
CC sequence given in the specification.
XX
SQ Sequence 54 BP; 10 A; 14 C; 19 G; 11 T; 0 other;

Query Match 67.0%; Score 13.4; DB 19; Length 54;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tgaccaagcttggca 15
||||||||||| |||
Db 21 TGACCAAGCTTAGCA 7

RESULT 15
AAF31402/c
ID AAF31402 standard; DNA; 54 BP.
XX
AC AAF31402;
XX
DT 10-APR-2001 (first entry)
XX
DE Oligonucleotide.
XX
KW Hemoglobin; globin; oxygen carrier; ss.
XX
OS Unidentified.
XX
PN US6172039-B1.
XX
PD 09-JAN-2001.
XX
PF 05-JUN-1995; 95US-0463160.
XX
PR 29-DEC-1994; 94US-0368407.
PR 07-JUN-1995; 95US-0484686.
PR 29-APR-1992; 92US-0876290.
PR 16-APR-1990; 90US-0509918.
PR 14-NOV-1990; 90US-0614359.
PR 12-APR-1991; 91US-0684611.
XX
PA (APEX-) APEX BIOSCIENCE INC.
XX
PI De Angelo J, Motwani NM, Bajwa W, Bonaventura J;
XX
DR WPI; 2001-136882/14.
XX
PT Novel globin chain in combination with a source of heme useful for
PT producing hemoglobin, is free of erythrocyte membrane component,
PT mammalian cell components and Escherichia coli endotoxins -
XX
PS Disclosure; Column 95; 144pp; English.
XX
CC The present invention relates to a substantially pure globin
CC chain which is free of erythrocyte membrane components,
CC Escherichia coli endotoxins and mammalian cell components.
CC The globin combined with a source of heme is useful for producing
CC hemoglobin, which in turn is useful as physiological oxygen carrier in
CC blood substitute solutions and in plasma expanders or in applications
CC requiring a physiological oxygen carrier.
XX
SQ Sequence 54 BP; 10 A; 14 C; 19 G; 11 T; 0 other;

Query Match 67.0%; Score 13.4; DB 22; Length 54;

Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 tgaccaagcttggca 15
           ||||||||||| |||
Db      21 TGACCAAGCTTAGCA 7
```

Search completed: March 13, 2002, 09:50:31
Job time: 5140 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 09:50:28 ; Search time 1263.07 Seconds
(without alignments)
13.575 Million cell updates/sec

Title: US-09-923-515-14
Perfect score: 20
Sequence: 1 gaccaagcttggcaggttct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	26	20	AAX89305	Primer used in RT-
c 2	13.8	69.0	20	20	AAZ31293	CCR5 gene inhibiti
c 3	13.8	69.0	36	20	AAX36413	PCR primer for IFN
c 4	13.8	69.0	36	20	AAX16122	PCR primer used in
c 5	13.8	69.0	36	22	AAF25939	Canine gamma inter
6	13.8	69.0	49	21	AAC99322	Human serum albumi
7	13.8	69.0	49	21	AAC99469	Human serum albumi
c 8	13.8	69.0	50	21	AAC99321	Human serum albumi
c 9	13.8	69.0	50	21	AAC99468	Human serum albumi
10	13.4	67.0	24	19	AAV43309	PCR primer used to
c 11	13.4	67.0	34	18	AAT60277	IGF-BP3 gene p53-b
12	13.4	67.0	34	18	AAT60279	IGF-BP3 gene p53-b
13	13.2	66.0	28	17	AAT39681	Primer #2 for chlo
14	13.2	66.0	28	19	AAV36601	Nucleotide sequenc
15	13.2	66.0	40	18	AAT61665	Antibody expressio
16	12.8	64.0	21	15	AAQ78742	Murine anti-human
17	12.8	64.0	21	19	AAV53747	Nucleotide sequenc
18	12.8	64.0	33	21	AAA11151	Primer 6456 for hu
19	12.8	64.0	33	21	AAA12609	PCR primer 6456 us
20	12.8	64.0	42	21	AAZ88412	H. pylori antigen
21	12.8	64.0	44	22	AAF56975	FIV gene cloning f
22	12.8	64.0	57	17	AAT12257	Cytochrome P450 CY
23	12.6	63.0	20	20	AAZ05125	PCR primer used to
c 24	12.6	63.0	22	21	AAA27233	Reverse PCR primer
c 25	12.6	63.0	22	21	AAA30354	FGFR3 mRNA PCR pri
26	12.6	63.0	28	8	AAN70798	DNA encoding mutan
c 27	12.6	63.0	30	19	AAV41483	Human alpha-1-AT m
28	12.6	63.0	31	21	AAC81892	A. thaliana SRp30
29	12.6	63.0	33	19	AAV39953	Streptococcus pneu
c 30	12.6	63.0	35	21	AAC64260	Soybean cotyledon
31	12.6	63.0	40	22	AAF81255	rbcL 3'-untranslat
32	12.6	63.0	40	22	AAF81336	rbcL 3'-untranslat
c 33	12.6	63.0	48	21	AAZ89637	HIV-2 ROD isolate
c 34	12.4	62.0	15	17	AAT37608	Apo(a) mRNA (nt. p
35	12.4	62.0	20	21	AAA98818	HPV18 specific pri
36	12.4	62.0	20	22	AAH42683	Primer and probe f
37	12.4	62.0	24	21	AAA38088	Oligonucleotide OD
38	12.4	62.0	24	21	AAA14544	Primer ODN-RT(-) w
39	12.4	62.0	24	21	AAA14553	Oligonucleotide 3'
40	12.4	62.0	24	22	AAS02282	Moloney murine leu
41	12.4	62.0	24	22	AAS02674	Oligodeoxynucleoti
42	12.4	62.0	28	18	AAT61292	Mouse integrin bet
c 43	12.4	62.0	31	17	AAT14227	Patched gene PCR p
c 44	12.4	62.0	31	19	AAV21638	Mouse patched (ptc
c 45	12.4	62.0	31	20	AAV64097	Mouse patched gene

ALIGNMENTS

RESULT 1
AAX89305
ID AAX89305 standard; DNA; 26 BP.
XX
AC AAX89305;
XX
DT 21-SEP-1999 (first entry)
XX
DE Primer used in RT-PCR analysis of transgenic apo(a).
XX
KW Transgenic rabbit; apolipoprotein (a); apolipoprotein B; lipoprotein;
KW atherosclerotic lesion; cholesterol; vascular injury; restenosis; apoB;
KW RT-PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9935241-A1.
XX
PD 15-JUL-1999.
XX
PF 08-JAN-1999; 99WO-US00401.
XX
PR 08-JAN-1998; 98US-0070727.
XX
PA (RHON) RHONE-POULENC RORER PHARM INC.
XX
PI Denefle P, Duverger N, Emmanuel F, Houdebine L;
PI Hughes SD, Rouy D, Rubin E, Viglietta C;
XX
DR WPI; 1999-430386/36.
XX
PT A transgenic rabbit that expresses a functional human lipoprotein A
XX
PS Example 3; Page 46; 73pp; English.

100%

```
XX
CC   The invention provides a transgenic rabbit, which has in its genomic
CC   DNA, sequences that encode apolipoprotein (a) and apolipoprotein B
CC   polypeptides, which are capable of combining to produce lipoprotein (a).
CC   The transgenic rabbit expresses a functional human lipoprotein (a). The
CC   rabbit develops human-like atherosclerotic lesions when fed a
CC   cholesterol rich diet. The transgenic rabbit is useful as a model for
CC   human diseases that are induced and/or exacerbated by lipoprotein (a)
CC   expression. The model can be used to identify inhibitors of lipoprotein
CC   (a) particle assembly and inhibitors of lipoprotein (a) associated
CC   diseases. The rabbit model is advantageous, when compared to the mouse,
CC   due partly to its relatively larger size, enabling facile studies of
CC   vascular injury and restenosis. In addition, while rabbits are similar to
CC   mice in lacking apo(a) and lipoprotein (a), their lipoprotein profile
CC   more closely mimics that of humans, with LDL as the predominant plasma
CC   lipoprotein. Sequences AAX89305-308 represent priomers used in the
CC   analysisi of transgenic apo(a) and apoB.
XX
SQ   Sequence 26 BP; 5 A; 7 C; 7 G; 7 T; 0 other;


  Query Match             100.0%;  Score 20;  DB 20;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.86;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 gaccaagcttggcaggttct 20
           ||||||||||||||||||||
Db       4 gaccaagcttggcaggttct 23


RESULT   2
AAZ31293/c
ID   AAZ31293 standard; DNA; 20 BP.
XX
AC   AAZ31293;
XX
DT   24-JAN-2000  (first entry)
XX
DE   CCR5 gene inhibiting antisense oligo AS(s)-50.
XX
KW   HIV cofactor inhibitor; HIV infection; CXCR4 gene; CCR5 gene;
KW   drug composition; antisense; ss.
XX
OS   Synthetic.
XX
PN   WO9951751-A1.
XX
PD   14-OCT-1999.
XX
PF   01-APR-1999;   99WO-JP01722.
XX
PR   02-APR-1998;   98JP-0125452.
XX
PA   (MARI-) MARINE BIO CO LTD.
XX
PI   Takaku H,  Yamamoto N,  Kimura T,  Takai K,  Wada A;
XX
DR   WPI; 1999-620207/53.
XX
PT   Antisense oligonucleotide-based HIV cofactor inhibitors, as drug
PT   compositions for treatment of HIV infection  -
XX
PS   Claim 6; Page 16; 59pp; Japanese.
XX
CC   The invention provides HIV cofactor inhibitors that contain
CC   oligonucleotides with a base sequence complementary to the CXCR4 or CCR5
CC   genes. Such inhibitors can be formulated into drug compositions for
CC   prevention or treatment of HIV infection, with inhibition of expression
CC   of CXCR4 or/and CCR5 gene. Sequences AAZ31244-306 represent antisense
CC   oligonucleotides to the CCR5 gene.
XX
SQ   Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 20;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 9.3e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 gaccaagcttggcaggt 17
           |||||||||  ||||||
Db      19 GACCAAGCTATGCAGGT 3


RESULT   3
AAX36413/c
ID   AAX36413 standard; DNA; 36 BP.
XX
AC   AAX36413;
XX
DT   06-JUL-1999  (first entry)
XX
DE   PCR primer for IFN-gamma coding sequence.
XX
KW   Interferon-gamma; IFN-gamma; recombinant baculovirus; silkworm larvae;
KW   IFN-gamma production; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP11098997-A.
XX
PD   13-APR-1999.
XX
PF   30-JUL-1998;   98JP-0216310.
XX
PR   01-AUG-1997;   97JP-0208087.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-295324/25.
XX
PT   Preparation of interferon-gamma - using recombinant baculovirus and
PT   silkworm larvae
XX
PS   Example 1; Page 8; 12pp; Japanese.
XX
CC   This sequence represents a PCR primer for DNA encoding an
CC   interferon-gamma (IFN-gamma) protein.
CC   The invention relates to a method for the preparation of IFN-gamma by
CC   inactivation of recombinant baculovirus under acidic or alkaline
CC   conditions contained in a cultured supernatant of cultured insect cells
CC   infected with a recombinant virus with a DNA encoding for protein of
CC   IFN-gamma, or in body fluid extract of silkworm larvae infected with the
CC   baculovirus. The method allows for the mass production of IFN-gamma at
CC   low cost.
XX
SQ   Sequence 36 BP; 8 A; 8 C; 10 G; 10 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 20;  Length 36;
  Best Local Similarity   88.2%;  Pred. No. 9.7e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 caagcttggcaggttct 20
           || ||||||||  |||||
Db      31 CATGCTTGGCAAGTTCT 15


RESULT   4
AAX16122/c
ID   AAX16122 standard; DNA; 36 BP.
XX
AC   AAX16122;
XX
DT   25-MAY-1999  (first entry)
XX
DE   PCR primer used in the course of the invention.
```

XX
KW Protein stabilization; arabic acid; storage stability; cytokine;
KW injectable drug composition; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9906429-A1.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-JP03431.
XX
PR 25-DEC-1997; 97JP-0357872.
PR 01-AUG-1997; 97JP-0208085.
PR 01-AUG-1997; 97JP-0208086.
XX
PA (TORA) TORAY IND INC.
XX
PI Hara N, Ito T, Okano F, Satoh M, Watanabe M, Yamada K;
PI Yanai A;
XX
DR WPI; 1999-153694/13.
XX
PT Stabilisation of proteins, e.g. cytokines - by mixing with aqueous
PT solution of arabic acid-type compound to give useful protein
PT composition
XX
PS Example 1; Page 64; 78pp; Japanese.
XX
CC The present PCR primer was used in the course of the invention. The
CC specification describes a method for the stabilizing proteins. The
CC method comprises mixing the protein with an aqueous solution of a
CC compound having a basic structure of arabic acid. The method is used
CC to provide storage stability of proteins such as cytokines, e.g. as
CC injectable drug compositions.
XX
SQ Sequence 36 BP; 8 A; 8 C; 10 G; 10 T; 0 other;

Query Match 69.0%; Score 13.8; DB 20; Length 36;
Best Local Similarity 88.2%; Pred. No. 9.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 caagcttggcaggttct 20
|| |||||||| |||||
Db 31 CATGCTTGGCAAGTTCT 15

RESULT 5
AAF25939/c
ID AAF25939 standard; DNA; 36 BP.
XX
AC AAF25939;
XX
DT 19-APR-2001 (first entry)
XX
DE Canine gamma interferon primer SEQ ID NO 9.
XX
KW *Canine; gamma interferon; IFN-gamma; mutant; dog; antiinflammatory;*
KW silkworm nuclear polyhederosis virus; intractable canine dermatitis;
KW primer; ss.
XX
OS Canis sp.
XX
PN JP2000316585-A.
XX
PD 21-NOV-2000.
XX
PF 09-JUN-1999; 99JP-0162320.
XX
PR 09-JUN-1998; 98JP-0160627.
PR 08-MAR-1999; 99JP-0059604.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 2001-184972/19.
XX
PT New canine interferon-gamma mutant, useful for treating intractable
PT canine dermatitis -
XX
PS Example 1; Page 13; 26pp; Japanese.
XX
CC This invention describes a novel canine interferon-gamma mutant (I). The
CC invention also describes (1) a gene (II) encoding (I); (2) preparation of
CC (I) in which the sugar chain-combined site is removed; (3) preparation
CC (M1) of (I) in which a recombinant silkworm nuclear polyhederosis virus
CC gene recombined by (I) is grown in a silkworm established cell or a
CC silkworm living body; and (4) an agent for treating intractable canine
CC dermatitis containing (I) prepared by M1. The products of the invention
CC have dermatological and antiinflammatory activity.
XX
SQ Sequence 36 BP; 8 A; 8 C; 10 G; 10 T; 0 other;

Query Match 69.0%; Score 13.8; DB 22; Length 36;
Best Local Similarity 88.2%; Pred. No. 9.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 caagcttggcaggttct 20
|| |||||||| |||||
Db 31 CATGCTTGGCAAGTTCT 15

RESULT 6
AAC99322
ID AAC99322 standard; DNA; 49 BP.
XX
AC AAC99322;
XX
DT 07-MAR-2001 (first entry)
XX
DE Human serum albumin (HSA) related oligonucleotide A-9.
XX
KW Human serum albumin; HSA; ss.
XX
OS Homo sapiens.
XX
PN CN1266099-A.
XX
PD 13-SEP-2000.
XX
PF 04-MAR-1999; 99CN-0102745.
XX
PR 04-MAR-1999; 99CN-0102745.
XX
PA (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI Liu Z;
XX
DR WPI; 2000-673206/66.
XX
PT Novel methods for chemical synthesis, expression and recombinant
PT protein production for human serum albumin reformed gene -
XX
PS Example 2; Fig 8; 85pp; Chinese.
XX
CC The present invention relates to two kinds of DNA sequences of coded
CC human serum albumin (HSA), i.e. design of structure-modified gene
CC segment of HSA and artificial total synthesis and a production process
CC for large-scale production of genetic recombinant HSA by using
CC methanol, yeast and engineering bacterium, and discovers that the
CC structure-modified gene can greatly increase the expression quantity
CC of HSA. The production process can make the structural gene of HSA
CC obtain high-level expression under the drive of promoter induced by
CC methanol, and make the HSA expression product secrete into the
CC fermenting liquor culture medium, and provide reliable test data for

```
CC   more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC   to AAC99391 represent oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 49 BP; 7 A; 11 C; 12 G; 19 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 21;  Length 49;
  Best Local Similarity   88.2%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 accaagcttggcaggtt 18
          ||||| ||||||| |||
Db     16 accaatcttggcaagtt 32


RESULT   7
AAC99469
ID   AAC99469 standard; DNA; 49 BP.
XX
AC   AAC99469;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human serum albumin (HSA) related oligonucleotide A-9.
XX
KW   Human serum albumin; HSA; ss.
XX
OS   Homo sapiens.
XX
PN   CN1266100-A.
XX
PD   13-SEP-2000.
XX
PF   04-MAR-1999;   99CN-0102794.
XX
PR   04-MAR-1999;   99CN-0102794.
XX
PA   (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI   Liu Z;
XX
DR   WPI; 2000-673207/66.
XX
PT   Novel methods for the chemical synthesis, expression and recombinant
PT   protein production for human serum albumin reformed gene -
XX
PS   Example 2; Fig 8; 85pp; Chinese.
XX
CC   The present invention relates to two kinds of DNA sequences of coded
CC   human serum albumin (HSA), i.e. design of structure-modified gene
CC   segment of HSA and artificial total synthesis and a production process
CC   for large-scale production of genetic recombinant HSA by using
CC   methanol, yeast and engineering bacterium, and discovers that the
CC   structure-modified gene can greatly increase the expression quantity
CC   of HSA. The production process can make the structural gene of HSA
CC   obtain high-level expression under the drive of promoter induced by
CC   methanol, and make the HSA expression product secrete into the
CC   fermenting liquor culture medium, and provide reliable test data for
CC   more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC   to AAC99391 represent oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 49 BP; 7 A; 11 C; 12 G; 19 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 21;  Length 49;
  Best Local Similarity   88.2%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 accaagcttggcaggtt 18
          ||||| ||||||| |||
Db     16 accaatcttggcaagtt 32


RESULT   8
AAC99321/c
ID   AAC99321 standard; DNA; 50 BP.
XX
AC   AAC99321;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human serum albumin (HSA) related oligonucleotide A-8.
XX
KW   Human serum albumin; HSA; ss.
XX
OS   Homo sapiens.
XX
PN   CN1266099-A.
XX
PD   13-SEP-2000.
XX
PF   04-MAR-1999;   99CN-0102745.
XX
PR   04-MAR-1999;   99CN-0102745.
XX
PA   (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI   Liu Z;
XX
DR   WPI; 2000-673206/66.
XX
PT   Novel methods for chemical synthesis, expression and recombinant
PT   protein production for human serum albumin reformed gene -
XX
PS   Example 2; Fig 8; 85pp; Chinese.
XX
CC   The present invention relates to two kinds of DNA sequences of coded
CC   human serum albumin (HSA), i.e. design of structure-modified gene
CC   segment of HSA and artificial total synthesis and a production process
CC   for large-scale production of genetic recombinant HSA by using
CC   methanol, yeast and engineering bacterium, and discovers that the
CC   structure-modified gene can greatly increase the expression quantity
CC   of HSA. The production process can make the structural gene of HSA
CC   obtain high-level expression under the drive of promoter induced by
CC   methanol, and make the HSA expression product secrete into the
CC   fermenting liquor culture medium, and provide reliable test data for
CC   more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC   to AAC99391 represent oligonucleotides used in the exemplification of
CC   the present invention.
XX
SQ   Sequence 50 BP; 20 A; 13 C; 11 G; 6 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 21;  Length 50;
  Best Local Similarity   88.2%;  Pred. No. 1e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 accaagcttggcaggtt 18
          ||||| ||||||| |||
Db     39 ACCAATCTTGGCAAGTT 23


RESULT   9
AAC99468/c
ID   AAC99468 standard; DNA; 50 BP.
XX
AC   AAC99468;
XX
DT   07-MAR-2001  (first entry)
XX
DE   Human serum albumin (HSA) related oligonucleotide A-8.
XX
KW   Human serum albumin; HSA; ss.
XX
```

OS Homo sapiens.
XX
PN CN1266100-A.
XX
PD 13-SEP-2000.
XX
PF 04-MAR-1999; 99CN-0102794.
XX
PR 04-MAR-1999; 99CN-0102794.
XX
PA (MAOJ-) MAOJI BIOLOGICAL ENG SCI & TECH CO LTD.
XX
PI Liu Z;
XX
DR WPI; 2000-673207/66.
XX
PT Novel methods for the chemical synthesis, expression and recombinant
PT protein production for human serum albumin reformed gene -
XX
PS Example 2; Fig 8; 85pp; Chinese.
XX
CC The present invention relates to two kinds of DNA sequences of coded
CC human serum albumin (HSA), i.e. design of structure-modified gene
CC segment of HSA and artificial total synthesis and a production process
CC for large-scale production of genetic recombinant HSA by using
CC methanol, yeast and engineering bacterium, and discovers that the
CC structure-modified gene can greatly increase the expression quantity
CC of HSA. The production process can make the structural gene of HSA
CC obtain high-level expression under the drive of promoter induced by
CC methanol, and make the HSA expression product secrete into the
CC fermenting liquor culture medium, and provide reliable test data for
CC more large-scale pilot-amplification of gene engineering HSA. AAC99312
CC to AAC99391 represent oligonucleotides used in the exemplification of
CC the present invention.
XX
SQ Sequence 50 BP; 20 A; 13 C; 11 G; 6 T; 0 other;

Query Match 69.0%; Score 13.8; DB 21; Length 50;
Best Local Similarity 88.2%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 accaagcttggcaggtt 18
||||| ||||||| |||
Db 39 ACCAATCTTGGCAAGTT 23

RESULT 10
AAV43309
ID AAV43309 standard; DNA; 24 BP.
XX
AC AAV43309;
XX
DT 26-OCT-1998 (first entry)
XX
DE PCR primer used to amplify nucleic acid ligands for ICP4.
XX
KW ICP4; transcriptional regulator; Herpes simplex virus; HSV;
KW nucleic acid ligand; treatment; prevention; disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN US5795721-A.
XX
PD 18-AUG-1998.
XX
PF 25-JAN-1996; 96US-0591989.
XX
PR 25-JAN-1996; 96US-0591989.
PR 11-JUN-1990; 90US-0536428.
PR 10-JUN-1991; 91US-0714131.
PR 24-MAR-1995; 95US-0409442.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
PI Gold L, Jayasena SD, Rabin RS;
XX
DR WPI; 1998-466659/40.
XX
PT Identification of nucleic acid ligands to ICP4 protein family member
PT - comprises preparing candidate mixture of nucleic acids, contacting
PT candidate mixture of nucleic acids with ICP4, partitioning increased
PT affinity nucleic acids, and amplifying
XX
PS Example 1; Column 24; 36pp; English.
XX
CC PCR primers AAV43309-10 were used to amplify nucleic acid ligands of
CC ICP4, which were isolated using the SELEX (Systematic Evolution of
CC Ligands by Exponential enrichment) procedure. ICP4 is the major
CC transcriptional regulator of Herpes simplex virus (HSV) gene expression.
CC The specification describes a method for the identification of nucleic
CC acid ligands to an ICP4 protein family member (PFM), which uses the
CC SELEX procedure. The method is used to yield a mixture of nucleic acids
CC enriched for nucleic acid sequences with relatively higher affinity and
CC specificity for binding ICP4 protein family member. The nucleic acid
CC ligands identified are used in the treatment or prevention of diseases
CC or medical conditions in humans, specifically those caused by herpes
CC viruses. They may also be used in diagnostic procedures.
XX
SQ Sequence 24 BP; 6 A; 5 C; 10 G; 3 T; 0 other;

Query Match 67.0%; Score 13.4; DB 19; Length 24;
Best Local Similarity 93.3%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 accaagcttggcagg 16
||||||||||| |||
Db 1 accaagcttgggagg 15

RESULT 11
AAT60277/c
ID AAT60277 standard; DNA; 34 BP.
XX
AC AAT60277;
XX
DT 26-NOV-1997 (first entry)
XX
DE IGF-BP3 gene p53-binding element.
XX
KW Insulin-like growth factor binding protein-3; IGF-BP3; p53;
KW tumour suppressor; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_binding 10..29
FT /*tag= a
FT /note= "p53-binding element (nts 4078-4097)"
XX
PN WO9709998-A2.
XX
PD 20-MAR-1997.
XX
PF 12-SEP-1996; 96WO-US14623.
XX
PR 14-SEP-1995; 95US-0003730.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Buckbinder L, Kley NA, Seizinger BR;
XX
DR WPI; 1997-202005/18.
XX
PT Treatment of p53-related tumours - using insulin-like growth factor

```
PT   binding protein-3 or a modulator of its expression or activity
XX
PS   Claim 2; Page 10; 28pp; English.
XX
CC   This DNA sequence is a p53-binding DNA element found in intron 2
CC   (nts 4079-97) of the insulin-like growth factor binding protein-3
CC   (IGF-BP3) gene.  This, and another DNA element (see AAT60276), were
CC   determined by computer analysis to have similarity to the p53
CC   consensus binding site.  Claimed methods for treating p53-related
CC   tumours comprise administering a modulator of IGF-BP3 that
CC   upregulates IGF-BP3 expression or activity, administering IGF-BP3
CC   or administering an expression vector encoding IGF-BP3.  A method
CC   of identifying a substance useful in the treatment of p53-related
CC   tumours comprises (a) applying a test substance to a cell having
CC   an expression vector containing a reporter gene linked to one or
CC   both of the p53-binding elements from the IGF-BP3 gene, and (b)
CC   analysing the cell to detect expression of the reporter gene.
XX
SQ   Sequence 34 BP; 9 A; 8 C; 13 G; 4 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 18;  Length 34;
  Best Local Similarity   93.3%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 ccaagcttggcaggt 17
           ||| ||||||||||
Db      31 CCAGGCTTGGCAGGT 17


RESULT  12
AAT60279
ID   AAT60279 standard; DNA; 34 BP.
XX
AC   AAT60279;
XX
DT   26-NOV-1997  (first entry)
XX
DE   IGF-BP3 gene p53-binding element consensus competitor.
XX
KW   Insulin-like growth factor binding protein-3; IGF-BP3; p53;
KW   tumour suppressor; ds.
XX
OS   Synthetic.
XX
PN   WO9709998-A2.
XX
PD   20-MAR-1997.
XX
PF   12-SEP-1996;   96WO-US14623.
XX
PR   14-SEP-1995;   95US-0003730.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Buckbinder L,  Kley NA,  Seizinger BR;
XX
DR   WPI; 1997-202005/18.
XX
PT   Treatment of p53-related tumours - using insulin-like growth factor
PT   binding protein-3 or a modulator of its expression or activity
XX
PS   Disclosure; Page 10; 28pp; English.
XX
CC   A consensus competitor (AAT60279) and mutant competitor (AAT60280)
CC   were used in experiments for the characterisation of 2 p53-binding
CC   and -responsive elements (see AAT60276-77) found in the insulin-like
CC   growth factor binding protein-3 (IGF-BP3) gene.  The results
CC   demonstrated specific binding of p53 to the p53-binding elements
CC   and that the p53-binding elements confer p53-inducibility to a
CC   heterologous promoter.
XX
SQ   Sequence 34 BP; 4 A; 13 C; 8 G; 9 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 18;  Length 34;
  Best Local Similarity   93.3%;  Pred. No. 1.5e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 ccaagcttggcaggt 17
           ||| ||||||||||
Db       8 ccaggcttggcaggt 22


RESULT  13
AAT39681
ID   AAT39681 standard; cDNA; 28 BP.
XX
AC   AAT39681;
XX
DT   03-JUN-1997  (first entry)
XX
DE   Primer #2 for chloramphenicol resistance gene.
XX
KW   D-aminotransferase; Bacillus sphaericus; D-amino acid; alpha-keto acid;
KW   phenylpyruvate; D-phenylalanine; polymerase chain reaction; primer; PCR;
KW   amplify; transamination; ss.
XX
OS   Synthetic.
XX
PN   EP736604-A2.
XX
PD   09-OCT-1996.
XX
PF   30-MAR-1996;   96EP-0105167.
XX
PR   19-APR-1995;   95US-0424797.
PR   03-APR-1995;   95US-0415716.
XX
PA   (NUTR-) NUTRASWEET CO.
XX
PI   Fotheringham I,  Taylor PB,  Yoshida RK;
XX
DR   WPI; 1996-444891/45.
XX
PT   Prodn. of D-phenylalanine in E. coli - using recombinant E. coli
PT   contg. a new isolated gene encoding a Bacillus sphaericus
PT   D-amino:transferase
XX
PS   Example 2; Page 7; 24pp; English.
XX
CC   AAT39672-T39685 represent amplification primers used in the construction
CC   of vectors for use in the method of the invention.  The vectors contain
CC   the coding sequence for the D-aminotransferase of Bacillus sphaericus
CC   (see AAT39671).  D-aminotransferases reversibly catalyse the
CC   transamination of various D-amino acids and corresponding alpha-keto
CC   acids. The D-aminotransferase sequence was isolated by MboI digestion of
CC   B. sphaericus chromosomal DNA, transforming E. coli with the digested
CC   DNA, and analysing the DNA in transformants plated on appropriate medium
CC   (preferably a medium containing L-aspartic acid, L-alanine, and
CC   phenylpyruvate) that produced D-phenylalanine. The D-aminotransferase
CC   protein sequence is used for producing D-phenylalanine.  The method of
CC   the invention comprises incorporating one of the vectors constructed
CC   using these sequences into E. coli, culturing the microorganism in a
CC   culture medium and isolating the D-phenylalanine from the culture.  The
CC   method provides for the high level production of D-phenylalanine,
CC   particularly enantiomerically-pure D-phenylalanine.
XX
SQ   Sequence 28 BP; 6 A; 8 C; 9 G; 5 T; 0 other;


  Query Match             66.0%;  Score 13.2;  DB 17;  Length 28;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 ccaagcttggcaggttct 20
```

```
          ||||||||  |||| |||
Db      2 ccaagcttatcaggctct 19


RESULT  14
AAV36601
ID   AAV36601 standard; cDNA; 28 BP.
XX
AC   AAV36601;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Nucleotide sequence of PCR primer 10.
XX
KW   D-aminotransferase; dat; enantiomere; D-amino acid; D-phenylalanine;
KW   keto-acid precursor; PCR; primer; amplification; ss.
XX
OS   Synthetic.
XX
PN   US5728555-A.
XX
PD   17-MAR-1998.
XX
PF   30-SEP-1996;   96US-0723896.
XX
PR   30-SEP-1996;   96US-0723896.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Fotheringham IG,  Taylor PP,  Ton JL;
XX
DR   WPI; 1998-206568/18.
XX
PT   New cells containing exogenous D-amino:transferase and
PT   L-amino:deaminase gene - useful for production of enantiomerically
PT   pure D-amino acids, especially D-phenylalanine
XX
PS   Example 3; Column 13; 33pp; English.
XX
CC   This is the nucleotide sequence of the PCR primer used for
CC   amplification in the method of the invention, where recombinant cells
CC   containing D-aminotransferase (dat) are produced.  These cells are
CC   useful for the production of high yields of the enantiomerically pure,
CC   (non) natural D-amino acids, especially D-phenylalanine.  The cells
CC   are also capable of converting existing L-amino acids to the D-form
CC   and also carrying out their degradation to keto-acid precursors as
CC   substrates for the dat enzyme.
XX
SQ   Sequence 28 BP; 6 A; 8 C; 9 G; 5 T; 0 other;

  Query Match             66.0%;  Score 13.2;  DB 19;  Length 28;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      3 ccaagcttggcaggttct 20
          ||||||||  |||| |||
Db      2 ccaagcttatcaggctct 19


RESULT  15
AAT61665
ID   AAT61665 standard; DNA; 40 BP.
XX
AC   AAT61665;
XX
DT   18-NOV-1997  (first entry)
XX
DE   Antibody expression vector MCO5 fragment extension primer MC49.
XX
KW   Phage display vector; binding protein; Cre recombinase; antibody;
KW   polymerase chain reaction; combinatorial library; ss.
XX
OS   Synthetic.
XX
PN   WO9709436-A1.
XX
PD   13-MAR-1997.
XX
PF   05-SEP-1996;   96WO-AU00555.
XX
PR   05-SEP-1995;   95AU-0005239.
XX
PA   (CRCB-) CRC BIOPHARMACEUTICAL RES PTY LTD.
XX
PI   Hawkins NJ,  Vancov T,  Ward RL,  Zahra D;
XX
DR   WPI; 1997-192911/17.
XX
PT   Producing a phage display vector expressing both chains of a binding
PT   protein - involves site-specific recombination between a vector
PT   encoding one polypeptide chain and a vector encoding the other chain
PT   and Cre recombinase
XX
PS   Examples; Page 17; 41pp; English.
XX
CC   A new method has been developed for producing a phage display vector
CC   (PDV). The method involves recombining: (a) a vector including a
CC   sequence encoding a polypeptide chain of a specific binding pair member
CC   and (b) a phage vector including a sequence encoding Cre recombinase
CC   operatively linked to a control sequence allowing its expression; and a
CC   sequence encoding a second polypeptide chain of a specific binding pair
CC   member, in which one of the polypeptide chains is fused to and displayed
CC   at the surface of a component of a replicable genetic display package,
CC   where recombination produces a PDV including sequences encoding both
CC   polypeptide chains and where Cre recombinase expression is substantially
CC   inhibited. The present sequence represents a primer MC49 used to extend
CC   the ends of the antibody expression vector fragment MCO5, for use in the
CC   construction of Term-LacVH cassette. Antibodies displayed on the PDV
CC   surface can have a desired antigen specificity. The PDV are suitable for
CC   preparing combinatorial libraries of antibodies. Stable recombinants are
CC   produced, compared with prior art in which the recombination process is
CC   reversible. The inclusion of a selectable marker allows easier selection
CC   of recombinants and large antibody libraries can be generated.
XX
SQ   Sequence 40 BP; 13 A; 9 C; 6 G; 12 T; 0 other;

  Query Match             66.0%;  Score 13.2;  DB 18;  Length 40;
  Best Local Similarity   83.3%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      3 ccaagcttggcaggttct 20
          ||||||||||  | |  |||
Db      2 ccaagcttgggaagatct 19


Search completed: March 13, 2002, 09:50:29
Job time: 5138 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 09:50:20 ; Search time 1263.07 Seconds
(without alignments)
13.575 Million cell updates/sec

Title: US-09-923-515-9
Perfect score: 20
Sequence: 1 aagcttggcaggttcttcct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		19	95.0	26	20	AAX89305	Primer used in RT-
c 2		14.8	74.0	50	22	AAH89851	Human coding sequ
c 3		14.8	74.0	51	22	AAH89850	Human coding sequ
4		14.2	71.0	31	21	AAC81892	A. thaliana SRp30
5		14.2	71.0	33	20	AAV72949	Rat Munc13-1 PCR p
6		14.2	71.0	33	20	AAV72986	Rat Munc13-1 PCR p
7		14.2	71.0	33	20	AAV72974	Human Doc2-alpha P
c 8		14.2	71.0	36	20	AAX36413	PCR primer for IFN
c 9		14.2	71.0	36	20	AAX16122	PCR primer used in
c 10		14.2	71.0	36	22	AAF25939	Canine gamma inter
11		13.6	68.0	36	16	AAT34344	3' glaA noncoding
c 12		13.6	68.0	38	17	AAT11755	Probe for human ky
13		13.6	68.0	40	18	AAT61665	Antibody expressio
14		13.6	68.0	53	21	AAA62775	Endoglucanase PCR
c 15		13.6	68.0	54	16	AAQ97476	H. parainfluenza 2
c 16		13.4	67.0	15	17	AAT37608	Apo(a) mRNA (nt. p
c 17		13.2	66.0	26	16	AAT34345	3' glaA noncoding
18		13.2	66.0	29	19	AAV58774	Human secreted pro
19		13.2	66.0	42	17	AAT08934	Forward primer for
20		13.2	66.0	42	19	AAV66290	5' PCR primer for
21		13.2	66.0	42	19	AAV56253	HGV forward primer
22		13.2	66.0	42	20	AAX16481	PCR primer used to
23		13.2	66.0	42	20	AAX02528	US5856134 Seq ID 2
24		13.2	66.0	42	20	AAV82224	Hepatitis G virus
c 25		13.2	66.0	46	16	AAT15944	Cystic fibrosis-as
26		12.8	64.0	25	20	AAX88714	Detector oligonucl
27		12.8	64.0	25	21	AAA60951	Detector oligonucl
28		12.8	64.0	25	21	AAA57470	Detector oligonucl
29		12.8	64.0	25	22	AAF31212	High throughput as
c 30		12.8	64.0	60	20	AAX88713	RNA mimic oligonuc
c 31		12.8	64.0	60	21	AAA60950	Mouse GAPDH RNA mi
c 32		12.8	64.0	60	21	AAA57469	Mimic of the muri
c 33		12.8	64.0	60	22	AAF31211	High throughput
34		12.6	63.0	21	22	AAH62424	HERC1 polymorphi
c 35		12.6	63.0	25	21	AAC66766	Forward IL-12 geno
c 36		12.6	63.0	33	12	AAQ12101	Sequence encoding
c 37		12.6	63.0	33	12	AAQ12125	"Hydrophobic tail"
38		12.6	63.0	33	19	AAV11538	Recombinant MPO DN
c 39		12.6	63.0	34	18	AAT60277	IGF-BP3 gene p53-b
40		12.6	63.0	34	18	AAT60279	IGF-BP3 gene p53-b
c 41		12.6	63.0	36	18	AAX83113	Intron-exon juncti
42		12.6	63.0	38	21	AAA49212	pHD421 luciferase
43		12.6	63.0	43	16	AAQ96205	Human immunodefici
44		12.6	63.0	43	21	AAC62734	HIV RT gene 5' pri
c 45		12.6	63.0	46	21	AAC66768	T7 forward IL-12 g

ALIGNMENTS

RESULT 1
AAX89305
ID AAX89305 standard; DNA; 26 BP.
XX
AC AAX89305;
XX
DT 21-SEP-1999 (first entry)
XX
DE Primer used in RT-PCR analysis of transgenic apo(a).
XX
KW Transgenic rabbit; apolipoprotein (a); apolipoprotein B; lipoprotein;
KW atherosclerotic lesion; cholesterol; vascular injury; restenosis; apoB;
KW RT-PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9935241-A1.
XX
PD 15-JUL-1999.
XX
PF 08-JAN-1999; 99WO-US00401.
XX
PR 08-JAN-1998; 98US-0070727.
XX
PA (RHON) RHONE-POULENC RORER PHARM INC.
XX
PI Denefle P, Duverger N, Emmanuel F, Houdebine L;
PI Hughes SD, Rouy D, Rubin E, Viglietta C;
XX
DR WPI; 1999-430386/36.
XX
PT A transgenic rabbit that expresses a functional human lipoprotein A
XX
PS Example 3; Page 46; 73pp; English.

XX
CC The invention provides a transgenic rabbit, which has in its genomic
CC DNA, sequences that encode apolipoprotein (a) and apolipoprotein B
CC polypeptides, which are capable of combining to produce lipoprotein (a).
CC The transgenic rabbit expresses a functional human lipoprotein (a). The
CC rabbit develops human-like atherosclerotic lesions when fed a
CC cholesterol rich diet. The transgenic rabbit is useful as a model for
CC human diseases that are induced and/or exacerbated by lipoprotein (a)
CC expression. The model can be used to identify inhibitors of lipoprotein
CC (a) particle assembly and inhibitors of lipoprotein (a) associated
CC diseases. The rabbit model is advantageous, when compared to the mouse,
CC due partly to its relatively larger size, enabling facile studies of
CC vascular injury and restenosis. In addition, while rabbits are similar to
CC mice in lacking apo(a) and lipoprotein (a), their lipoprotein profile
CC more closely mimics that of humans, with LDL as the predominant plasma
CC lipoprotein. Sequences AAX89305-308 represent priomers used in the
CC analysisi of transgenic apo(a) and apoB.
XX
SQ Sequence 26 BP; 5 A; 7 C; 7 G; 7 T; 0 other;

Query Match 95.0%; Score 19; DB 20; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 aagcttggcaggttcttcc 19
||||||||||||||||||
Db 8 aagcttggcaggttcttcc 26

RESULT 2
AAH89851/c
ID AAH89851 standard; DNA; 50 BP.
XX
AC AAH89851;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 632.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
XX
OS Homo sapiens.
XX
PN WO200151670-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US00322.
XX
PR 07-JAN-2000; 2000US-0174962.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2001-451871/48.
DR P-PSDB; AAM00732.
XX
PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes -
XX
PS Claim 1; Page 287; 475pp; English.
XX
CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention.
XX
SQ Sequence 50 BP; 12 A; 14 C; 15 G; 9 T; 0 other;

Query Match 74.0%; Score 14.8; DB 22; Length 50;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 agcttggcaggttcttcc 19
|||||||||| ||| |||
Db 48 AGCTTGGCAGCTTCATCC 31

RESULT 3
AAH89850/c
ID AAH89850 standard; DNA; 51 BP.
XX
AC AAH89850;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human coding sequence polymorphic site SEQ ID NO: 631.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
XX
OS Homo sapiens.
XX
PN WO200151670-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US00322.
XX
PR 07-JAN-2000; 2000US-0174962.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2001-451871/48.
DR P-PSDB; AAM00731.
XX
PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes -
XX
PS Claim 1; Page 286; 475pp; English.
XX
CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention.
XX
SQ Sequence 51 BP; 12 A; 14 C; 16 G; 9 T; 0 other;

Query Match 74.0%; Score 14.8; DB 22; Length 51;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 agcttggcaggttcttcc 19

```
          |||||||||| ||| |||
Db     49 AGCTTGGCAGCTTCATCC 32


RESULT   4
AAC81892
ID   AAC81892 standard; DNA; 31 BP.
XX
AC   AAC81892;
XX
DT   23-FEB-2001  (first entry)
XX
DE   A. thaliana SRp30 protein primer #11.
XX
KW   SR protein; splice-factor activity; plant; developmental behavior;
KW   flowering; crop plant; cereal; bean; rice; fruit; primer; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200065059-A1.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-AT00100.
XX
PR   23-APR-1999;   99AT-0000727.
XX
PA   (OSTP ) OESTERR FORSCH SEIBERSDORF.
XX
PI   Barta A,  Lopato S,  Kalyna M,  Dorner S;
XX
DR   WPI; 2000-687349/67.
XX
PT   Novel proteins with splice-factor activity in plants, useful e.g. for
PT   altering flowering time or development, and the nucleic acid that
PT   encodes it -
XX
PS   Example; Page 15; 67pp; German.
XX
CC   This invention describes a novel protein (I) with splice-factor activity
CC   in plants (I) modifies the choice of splice sites in many plant
CC   pre-mRNAs. (I) (also the nucleic acid that encodes them and related
CC   vectors or expression systems) are used: (i) to alter splice patterns in
CC   plants, or their parts; (ii) to alter developmental behavior of plants;
CC   and/or (iii) to delay flowering, particularly by at least 25% relative
CC   to the wild type, especially in crop plants such as cereals, beans, rice
CC   and fruit.
XX
SQ   Sequence 31 BP; 8 A; 8 C; 5 G; 10 T; 0 other;


  Query Match             71.0%;  Score 14.2;  DB 21;  Length 31;
  Best Local Similarity   84.2%;  Pred. No. 6.9e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 aagcttggcaggttcttcc 19
           |||||||| |  |||||||
Db       6 aagcttggtatcttcttcc 24


RESULT   5
AAV72949
ID   AAV72949 standard; DNA; 33 BP.
XX
AC   AAV72949;
XX
DT   04-MAR-1999  (first entry)
XX
DE   Rat Muncl3-1 PCR primer SEQ ID NO:8.
XX
KW   Muncl3; Doc2-alpha; interacting domain; screening; agonist; antagonist;
KW   calcium ion dependent secretion inhibitor; neurotransmitter; hormone;
KW   fusion protein; nervous disease; PCR primer; ss.
XX
OS   Synthetic.
OS   Rattus sp.
XX
PN   JP10313866-A.
XX
PD   02-DEC-1998.
XX
PF   15-MAY-1997;   97JP-0126118.
XX
PR   15-MAY-1997;   97JP-0126118.
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
DR   WPI; 1999-074148/07.
XX
PT   Screening for agonists or antagonists of binding between Doc2-alpha
PT   and Muncl3 - used to treat diseases of the nervous system
XX
PS   Example 3; Page 27; 33pp; Japanese.
XX
CC   The present invention describes a method of screening for agonists or
CC   antagonists of the binding between Doc2-alpha and Muncl3. The method
CC   comprises reacting Doc2-alpha or its homologue with Muncl3 or its
CC   homologue optionally in the presence of a test substance and selecting
CC   the substances which increase or decrease binding. Also described are:
CC   (1) an agonist or antagonist of the binding between Doc2-alpha and
CC   Muncl3 selected by the above method; (2) a vector expressing Doc2-alpha
CC   or its homologue used for inhibiting Ca ion-dependent secretion of a
CC   neurotransmitter or hormone; (3) a vector expressing Muncl3 or its
CC   homologue used for inhibiting Ca ion-dependent secretion of a
CC   neurotransmitter or hormone; (4) a fusion protein between Doc2-alpha or
CC   its homologue and a carrier protein; (5) a fusion protein between Muncl3
CC   or its homologue and a carrier protein; (6) a polypeptide containing
CC   amino acids 13-37 of the sequence of Doc2-alpha, which binds with Muncl3
CC   and comprises at most 90 amino acids; and (7) a polypeptide containing
CC   amino acids 851-1461 of the sequence of Muncl3, which binds with Doc2-
CC   alpha and comprises at most 904 amino acids. The agonist or antagonist
CC   can be used to treat diseases of the nervous system. The present
CC   sequence represents a PCR primer for rat Muncl3-1.
XX
SQ   Sequence 33 BP; 6 A; 11 C; 6 G; 10 T; 0 other;


  Query Match             71.0%;  Score 14.2;  DB 20;  Length 33;
  Best Local Similarity   84.2%;  Pred. No. 6.9e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 agcttggcaggttcttcct 20
           |||||||||| |||  |||
Db      12 agcttggcagtttcaccct 30


RESULT   6
AAV72986
ID   AAV72986 standard; DNA; 33 BP.
XX
AC   AAV72986;
XX
DT   04-MAR-1999  (first entry)
XX
DE   Rat Muncl3-1 PCR primer SEQ ID NO:45.
XX
KW   Muncl3; Doc2-alpha; interacting domain; screening; agonist; antagonist;
KW   calcium ion dependent secretion inhibitor; neurotransmitter; hormone;
KW   fusion protein; nervous disease; PCR primer; ss.
XX
OS   Synthetic.
OS   Rattus sp.
XX
PN   JP10313866-A.
XX
PD   02-DEC-1998.
```

XX
PF 15-MAY-1997; 97JP-0126118.
XX
PR 15-MAY-1997; 97JP-0126118.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
DR WPI; 1999-074148/07.
XX
PT Screening for agonists or antagonists of binding between Doc2-alpha
PT and Munc13 - used to treat diseases of the nervous system
XX
PS Example 7; Page 31; 33pp; Japanese.
XX
CC The present invention describes a method of screening for agonists or
CC antagonists of the binding between Doc2-alpha and Munc13. The method
CC comprises reacting Doc2-alpha or its homologue with Munc13 or its
CC homologue optionally in the presence of a test substance and selecting
CC the substances which increase or decrease binding. Also described are:
CC (1) an agonist or antagonist of the binding between Doc2-alpha and
CC Munc13 selected by the above method; (2) a vector expressing Doc2-alpha
CC or its homologue used for inhibiting Ca ion-dependent secretion of a
CC neurotransmitter or hormone; (3) a vector expressing Munc13 or its
CC homologue used for inhibiting Ca ion-dependent secretion of a
CC neurotransmitter or hormone; (4) a fusion protein between Doc2-alpha or
CC its homologue and a carrier protein; (5) a fusion protein between Munc13
CC or its homologue and a carrier protein; (6) a polypeptide containing
CC amino acids 13-37 of the sequence of Doc2-alpha, which binds with Munc13
CC and comprises at most 90 amino acids; and (7) a polypeptide containing
CC amino acids 851-1461 of the sequence of Munc13, which binds with Doc2-
CC alpha and comprises at most 904 amino acids. The agonist or antagonist
CC can be used to treat diseases of the nervous system. The present
CC sequence represents a PCR primer for rat Munc13-1.
XX
SQ Sequence 33 BP; 5 A; 12 C; 7 G; 9 T; 0 other;

Query Match 71.0%; Score 14.2; DB 20; Length 33;
Best Local Similarity 84.2%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 agcttggcaggttcttcct 20
||||||||||| ||| |||
Db 12 agcttggcagtttcaccct 30

RESULT 7
AAV72974
ID AAV72974 standard; DNA; 33 BP.
XX
AC AAV72974;
XX
DT 04-MAR-1999 (first entry)
XX
DE Human Doc2-alpha PCR primer SEQ ID NO:33.
XX
KW Munc13; Doc2-alpha; interacting domain; screening; agonist; antagonist;
KW calcium ion dependent secretion inhibitor; neurotransmitter; hormone;
KW fusion protein; nervous disease; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN JP10313866-A.
XX
PD 02-DEC-1998.
XX
PF 15-MAY-1997; 97JP-0126118.
XX
PR 15-MAY-1997; 97JP-0126118.
XX
PA (SHIO) SHIONOGI & CO LTD.
XX
DR WPI; 1999-074148/07.
XX
PT Screening for agonists or antagonists of binding between Doc2-alpha
PT and Munc13 - used to treat diseases of the nervous system
XX
PS Example 6; Page 30; 33pp; Japanese.
XX
CC The present invention describes a method of screening for agonists or
CC antagonists of the binding between Doc2-alpha and Munc13. The method
CC comprises reacting Doc2-alpha or its homologue with Munc13 or its
CC homologue optionally in the presence of a test substance and selecting
CC the substances which increase or decrease binding. Also described are:
CC (1) an agonist or antagonist of the binding between Doc2-alpha and
CC Munc13 selected by the above method; (2) a vector expressing Doc2-alpha
CC or its homologue used for inhibiting Ca ion-dependent secretion of a
CC neurotransmitter or hormone; (3) a vector expressing Munc13 or its
CC homologue used for inhibiting Ca ion-dependent secretion of a
CC neurotransmitter or hormone; (4) a fusion protein between Doc2-alpha or
CC its homologue and a carrier protein; (5) a fusion protein between Munc13
CC or its homologue and a carrier protein; (6) a polypeptide containing
CC amino acids 13-37 of the sequence of Doc2-alpha, which binds with Munc13
CC and comprises at most 90 amino acids; and (7) a polypeptide containing
CC amino acids 851-1461 of the sequence of Munc13, which binds with Doc2-
CC alpha and comprises at most 904 amino acids. The agonist or antagonist
CC can be used to treat diseases of the nervous system. The present
CC sequence represents a PCR primer for human Doc2-alpha.
XX
SQ Sequence 33 BP; 5 A; 12 C; 7 G; 9 T; 0 other;

Query Match 71.0%; Score 14.2; DB 20; Length 33;
Best Local Similarity 84.2%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 agcttggcaggttcttcct 20
||||||||||| ||| |||
Db 12 agcttggcagtttcaccct 30

RESULT 8
AAX36413/c
ID AAX36413 standard; DNA; 36 BP.
XX
AC AAX36413;
XX
DT 06-JUL-1999 (first entry)
XX
DE PCR primer for IFN-gamma coding sequence.
XX
KW Interferon-gamma; IFN-gamma; recombinant baculovirus; silkworm larvae;
KW IFN-gamma production; PCR primer; ss.
XX
OS Synthetic.
XX
PN JP11098997-A.
XX
PD 13-APR-1999.
XX
PF 30-JUL-1998; 98JP-0216310.
XX
PR 01-AUG-1997; 97JP-0208087.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-295324/25.
XX
PT Preparation of interferon-gamma - using recombinant baculovirus and
PT silkworm larvae
XX
PS Example 1; Page 8; 12pp; Japanese.
XX
CC This sequence represents a PCR primer for DNA encoding an
CC interferon-gamma (IFN-gamma) protein.

```
CC   The invention relates to a method for the preparation of IFN-gamma by
CC   inactivation of recombinant baculovirus under acidic or alkaline
CC   conditions contained in a cultured supernatant of cultured insect cells
CC   infected with a recombinant virus with a DNA encoding for protein of
CC   IFN-gamma, or in body fluid extract of silkworm larvae infected with the
CC   baculovirus. The method allows for the mass production of IFN-gamma at
CC   low cost.
XX
SQ   Sequence 36 BP; 8 A; 8 C; 10 G; 10 T; 0 other;


  Query Match             71.0%;  Score 14.2;  DB 20;  Length 36;
  Best Local Similarity   84.2%;  Pred. No. 7e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 aagcttggcaggttcttcc 19
           | ||||||||  ||||||  |
Db      30 ATGCTTGGCAAGTTCTTAC 12


RESULT   9
AAX16122/c
ID   AAX16122 standard; DNA; 36 BP.
XX
AC   AAX16122;
XX
DT   25-MAY-1999  (first entry)
XX
DE   PCR primer used in the course of the invention.
XX
KW   Protein stabilization; arabic acid; storage stability; cytokine;
KW   injectable drug composition; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9906429-A1.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-JP03431.
XX
PR   25-DEC-1997;   97JP-0357872.
PR   01-AUG-1997;   97JP-0208085.
PR   01-AUG-1997;   97JP-0208086.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Hara N,  Ito T,  Okano F,  Satoh M,  Watanabe M,  Yamada K;
PI   Yanai A;
XX
DR   WPI; 1999-153694/13.
XX
PT   Stabilisation of proteins, e.g. cytokines - by mixing with aqueous
PT   solution of arabic acid-type compound to give useful protein
PT   composition
XX
PS   Example 1; Page 64; 78pp; Japanese.
XX
CC   The present PCR primer was used in the course of the invention. The
CC   specification describes a method for the stabilizing proteins. The
CC   method comprises mixing the protein with an aqueous solution of a
CC   compound having a basic structure of arabic acid. The method is used
CC   to provide storage stability of proteins such as cytokines, e.g. as
CC   injectable drug compositions.
XX
SQ   Sequence 36 BP; 8 A; 8 C; 10 G; 10 T; 0 other;


  Query Match             71.0%;  Score 14.2;  DB 20;  Length 36;
  Best Local Similarity   84.2%;  Pred. No. 7e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 aagcttggcaggttcttcc 19
           | ||||||||  ||||||  |
Db      30 ATGCTTGGCAAGTTCTTAC 12


RESULT  10
AAF25939/c
ID   AAF25939 standard; DNA; 36 BP.
XX
AC   AAF25939;
XX
DT   19-APR-2001  (first entry)
XX
DE   Canine gamma interferon primer SEQ ID NO 9.
XX
KW   Canine; gamma interferon; IFN-gamma; mutant; dog; antiinflammatory;
KW   silkworm nuclear polyhederosis virus; intractable canine dermatitis;
KW   primer; ss.
XX
OS   Canis sp.
XX
PN   JP2000316585-A.
XX
PD   21-NOV-2000.
XX
PF   09-JUN-1999;   99JP-0162320.
XX
PR   09-JUN-1998;   98JP-0160627.
PR   08-MAR-1999;   99JP-0059604.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-184972/19.
XX
PT   New canine interferon-gamma mutant, useful for treating intractable
PT   canine dermatitis
XX
PS   Example 1; Page 13; 26pp; Japanese.
XX
CC   This invention describes a novel canine interferon-gamma mutant (I). The
CC   invention also describes (1) a gene (II) encoding (I); (2) preparation of
CC   (I) in which the sugar chain-combined site is removed; (3) preparation
CC   (M1) of (I) in which a recombinant silkworm nuclear polyhederosis virus
CC   gene recombined by (I) is grown in a silkworm established cell or a
CC   silkworm living body; and (4) an agent for treating intractable canine
CC   dermatitis containing (I) prepared by M1. The products of the invention
CC   have dermatological and antiinflammatory activity.
XX
SQ   Sequence 36 BP; 8 A; 8 C; 10 G; 10 T; 0 other;


  Query Match             71.0%;  Score 14.2;  DB 22;  Length 36;
  Best Local Similarity   84.2%;  Pred. No. 7e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 aagcttggcaggttcttcc 19
           | ||||||||  ||||||  |
Db      30 ATGCTTGGCAAGTTCTTAC 12


RESULT  11
AAT34344
ID   AAT34344 standard; DNA; 36 BP.
XX
AC   AAT34344;
XX
DT   04-OCT-1996  (first entry)
XX
DE   3' glaA noncoding primer AB4233, binds 2.2 kb 3' of stop codon.
XX
KW   Polymerase chain reaction; primer; amplify; PCR; acetamidase gene;
KW   amdS; Aspergillus nidulans; selection; transformation; glaA;
KW   filamentous fungi; marker gene; antibiotic; selection marker;
KW   glyceraldehyde-3-phosphate dehydrogenase; gpdA; amyloglucosidase; ss.
```

XX
OS Synthetic.
XX
PN EP635574-A1.
XX
PD 25-JAN-1995.
XX
PF 30-JUN-1994; 94EP-0201896.
XX
PR 23-JUL-1993; 93EP-0202195.
XX
PA (KONN) GIST-BROCADES NV.
XX
PI Selten GCM, Swinkels BW, Van Gorcom RFM;
XX
DR WPI; 1995-053686/08.
XX
PT Selection marker gene free recombinant strains, esp. filamentous
PT fungi, and methods for obtaining them - for improved selection
PT without use of antibiotics and with no undesired residual marker DNA
PT following transformation
XX
PS Example 3; Page 21; 109pp; English.
XX
CC The sequences given in AAT34343-46 are primers which were used in the
CC construction of the glaA gene integration vector pGBGLA53. pGBGLA53
CC contains the A. ficuum phytase gene under control of the A. niger
CC amyloglucosidase (glaA) gene flanked by 3' glaA non-coding sequences
CC to direct integration at the 3' glaA non-coding region. These primers
CC were used to amplify the entire glaA locus using the plasmid pAB6-1 as
CC template, and to fuse it to the phytase coding sequence. The resultant
CC vector was used in the method of the invention for the selection of
CC transformed filamentous fungi from which the marker gene has been
CC deleted. This selection system reduces the need for antibiotic
CC selection markers which give rise to an undesired spread of strains that
CC have become resistant to antibiotics.
XX
SQ Sequence 36 BP; 8 A; 8 C; 8 G; 12 T; 0 other;

Query Match 68.0%; Score 13.6; DB 16; Length 36;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 aagcttggcaggttcttcct 20
||||||| | || ||||| |
Db 15 aagcttgactgggtcttctt 34

RESULT 12
AAT11755/c
ID AAT11755 standard; DNA; 38 BP.
XX
AC AAT11755;
XX
DT 27-JUL-1996 (first entry)
XX
DE Probe for human kynurenine aminotransferase (KAT) sequence.
XX
KW Kynurenine aminotransferase; KAT; kynurenic acid; KYNA; kynurenine;
KW KYN; brain; NMDA receptor; glutamatergic function; ss.
XX
OS Synthetic.
XX
PN WO9601893-A1.
XX
PD 25-JAN-1996.
XX
PF 23-JUN-1995; 95WO-US07855.
XX
PR 07-JUL-1994; 94US-0271667.
XX
PA (PHAA) PHARMACIA SPA.
PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI Benatti L, Breton J, Mosca M, Okuno E, Schwarcz R;
PI Speciale C;
XX
DR WPI; 1996-097623/10.
XX
PT Isolated DNA encoding mammalian kynurenine amino:transferase (KAT) -
PT useful in gene therapy applications and for identifying KAT in brain
PT tissue
XX
PS Example 4; Page 21; 51pp; English.
XX
CC Sequences encoding Kynurenine aminotransferase (KAT) can be inserted
CC into vectors and subsequently cells and hence can be used for gene
CC therapy. The vector and host cells can be used for cerebral
CC implantation to where KAT can directly catalyse the production of
CC kynurenic acid (KYNA) from kynurenine (KYN). It is thought KYNA acts
CC as a negative endogenous modulator of cerebral glutamatergic
CC function. KYNA concentrations and the activity of KAT show an
CC increase with age. KAT inhibitors, by providing an increase of the
CC glutamatergic tone at the NMDA receptor, could be useful in
CC situations where NMDA receptor function is insufficient and/or KAT
CC activity and KYNA levels are abnormally enhanced. Hence they could
CC be particularly useful in the treatment of the pathological
CC consequences associated with the aging processes in the brain.
CC Three KAT clones are described in AAT11560, AAT11742-43. The human KAT
CC sequence was cloned using four primers (AAT11751-54). The primer
CC AAT11751 was used to produce a cDNA sequence from a KAT polyA+ RNA. The
CC cDNA sequence was then amplified using the primers described in
CC AAT11752-54. The cloned sequence was then identified using a probe
CC (AAT11755)
XX
SQ Sequence 38 BP; 9 A; 9 C; 11 G; 9 T; 0 other;

Query Match 68.0%; Score 13.6; DB 17; Length 38;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 aagcttggcaggttcttcct 20
|| |||| |||| ||||| |
Db 27 AAACTTGCCAGGATCTTCGT 8

RESULT 13
AAT61665
ID AAT61665 standard; DNA; 40 BP.
XX
AC AAT61665;
XX
DT 18-NOV-1997 (first entry)
XX
DE Antibody expression vector MCO5 fragment extension primer MC49.
XX
KW Phage display vector; binding protein; Cre recombinase; antibody;
KW polymerase chain reaction; combinatorial library; ss.
XX
OS Synthetic.
XX
PN WO9709436-A1.
XX
PD 13-MAR-1997.
XX
PF 05-SEP-1996; 96WO-AU00555.
XX
PR 05-SEP-1995; 95AU-0005239.
XX
PA (CRCB-) CRC BIOPHARMACEUTICAL RES PTY LTD.
XX
PI Hawkins NJ, Vancov T, Ward RL, Zahra D;
XX
DR WPI; 1997-192911/17.

XX
PT Producing a phage display vector expressing both chains of a binding
PT protein - involves site-specific recombination between a vector
PT encoding one polypeptide chain and a vector encoding the other chain
PT and Cre recombinase
XX
PS Examples; Page 17; 41pp; English.
XX
CC A new method has been developed for producing a phage display vector
CC (PDV). The method involves recombining: (a) a vector including a
CC sequence encoding a polypeptide chain of a specific binding pair member
CC and (b) a phage vector including a sequence encoding Cre recombinase
CC operatively linked to a control sequence allowing its expression; and a
CC sequence encoding a second polypeptide chain of a specific binding pair
CC member, in which one of the polypeptide chains is fused to and displayed
CC at the surface of a component of a replicable genetic display package,
CC where recombination produces a PDV including sequences encoding both
CC polypeptide chains and where Cre recombinase expression is substantially
CC inhibited. The present sequence represents a primer MC49 used to extend
CC the ends of the antibody expression vector fragment MC05, for use in the
CC construction of Term-LacVH cassette. Antibodies displayed on the PDV
CC surface can have a desired antigen specificity. The PDV are suitable for
CC preparing combinatorial libraries of antibodies. Stable recombinants are
CC produced, compared with prior art in which the recombination process is
CC reversible. The inclusion of a selectable marker allows easier selection
CC of recombinants and large antibody libraries can be generated.
XX
SQ Sequence 40 BP; 13 A; 9 C; 6 G; 12 T; 0 other;

Query Match 68.0%; Score 13.6; DB 18; Length 40;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 aagcttggcaggttcttcct 20
||||||| | | ||||| |
Db 4 aagcttgggaagatcttcat 23

RESULT 14
AAA62775
ID AAA62775 standard; DNA; 53 BP.
XX
AC AAA62775;
XX
DT 25-SEP-2000 (first entry)
XX
DE Endoglucanase PCR primer pMN-Bam.
XX
KW Endoglucanase; cellulose breakdown; produce pulp; papermaking;
KW animal foodstuff; primer; ss.
XX
OS Synthetic.
XX
PN WO200024879-A1.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-JP05884.
XX
PR 23-OCT-1998; 98JP-0302387.
XX
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
XX
PI Nakamura Y, Moriya T, Baba Y, Yanai K, Sumida N, Nishimura T;
PI Murashima K, Nakane A, Yaguchi T, Koga J, Murakami T, Kono T;
XX
DR WPI; 2000-365117/31.
XX
PT Endoglucanases of fungal origin with high activity under alkaline
PT conditions for production of paper pulp and animal feedstuffs -
XX
PS Claim 51; Page 58; 180pp; Japanese.
XX
CC This sequence represents a PCR primer used in the identification of an
CC endoglucanase encoding protein. The invention relates to an
CC endoglucanase of fungal origin which can completely break down purified
CC cellulose at a concentration of less than 1mg protein/litre, and produces
CC more than 50% breakdown of cellulose at pH 8.5. The invention includes
CC endoglucanase protein sequences (see AAB09825-B09830), endoglucanase
CC nucleotide sequences (see AAA62726-A62732) and primers (AAA62733-A62802)
CC which are used in the identification of the endoglucanase sequences, and
CC in the construction of vectors containing the polynucleotides. The
CC endoglucanase enzymes are used for the production of pulp for papermaking
CC and for the production of animal foodstuffs.
XX
SQ Sequence 53 BP; 13 A; 13 C; 14 G; 13 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 53;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 aagcttggcaggttcttcct 20
||| | | || |||||||||
Db 31 aagatggccaagttcttcct 50

RESULT 15
AAQ97476/c
ID AAQ97476 standard; RNA; 54 BP.
XX
AC AAQ97476;
XX
DT 13-MAR-1996 (first entry)
XX
DE H. parainfluenza 23S rRNA target sequence spanning bases 291-332.
XX
KW Probe; 16S; 23S; rRNA; rDNA; Haemophilus influenzae; detection; ss.
XX
OS Haemophilus parainfluenza.
XX
PN WO9520055-A1.
XX
PD 27-JUL-1995.
XX
PF 19-JAN-1995; 95WO-US00802.
XX
PR 21-JAN-1994; 94US-0184607.
XX
PA (STAD) AMOCO CORP.
XX
PI Shah J;
XX
DR WPI; 1995-269466/35.
XX
PT Nucleic acid probes specific for Haemophilus influenzae - for rapid
PT and accurate detection of H. influenza rRNA or rDNA
XX
PS Disclosure; Fig 2; 43pp; English.
XX
CC The sequences given in AAQ97472-82 represent regions from the 23S rRNA
CC from different microbacterial strains. These regions were used in the
CC design of probes which are specific for the 23S rRNA of Haemophilus
CC influenzae. The target region of the 23S rRNA is bounded by
CC nucleotide positions 343-356. The probes pref. bind to
CC DNA or RNA from H. influenzae in preference to other non-H. influenzae
CC organisms. These probes may be used to rapidly detect H. influenzae
CC infection, in a variety of inexpensive, easy-to-use assay systems
CC (see also AAQ96395-400).
XX
SQ Sequence 54 BP; 20 A; 10 C; 18 G; 1 T; 5 U; 0 other;

Query Match 68.0%; Score 13.6; DB 16; Length 54;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1 aagcttggcaggttcttcct 20
           ||||||  ||| || |||||
Db      34 AAGCTTCCCAGCTTGTTCCT 15
```

Search completed: March 13, 2002, 09:50:22
Job time: 5131 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 09:50:18 ; Search time 1263.07 Seconds
(without alignments)
13.575 Million cell updates/sec

Title: US-09-923-515-8
Perfect score: 20
Sequence: 1 tctgcgtctgagcattgcgt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	15	75.0	15	17	AAT37560	Apo(a) mRNA (nt. p
c	2	13.8	69.0	20	19	AAV23052	HG5647S-20 primer
c	3	13.4	67.0	53	21	AAC70054	VEGF-binding nucle
c	4	13.2	66.0	28	19	AAV64594	Human native inter
	5	13	65.0	51	21	AAA77044	Human clone cg4332
	6	13	65.0	51	21	AAA77045	Human clone cg4332
	7	12.8	64.0	26	22	AAH45651	PCR primer specifi
	8	12.6	63.0	20	20	AAX92916	PCR primer used to
c	9	12.6	63.0	22	21	AAA35410	Myrtaceae microsat
c	10	12.6	63.0	25	17	AAT30288	Nuclear polyhedros
c	11	12.6	63.0	25	18	AAT59325	DNA primer for Bac
c	12	12.6	63.0	31	22	AAI30310	Human single nucle
c	13	12.6	63.0	51	22	AAH89265	Human coding sequ
	14	12.4	62.0	20	13	AAQ32826	Microsatellite rep
	15	12.4	62.0	20	15	AAQ57849	Primer pair 19A HS
	16	12.4	62.0	20	18	AAT94357	Human DPC4 sequenc
c	17	12.4	62.0	51	21	AAA76588	Human clone cg2142
c	18	12.4	62.0	51	21	AAA76589	Human clone cg2142
	19	12.4	62.0	60	18	AAT92161	Human DPC4 in vitr
c	20	12.2	61.0	20	17	AAT39491	Steroidogenesis ac
	21	12.2	61.0	20	22	AAD07122	Canine TCTE1L micr
c	22	12.2	61.0	31	22	AAI30309	Human single nucle
c	23	12.2	61.0	37	17	AAT17826	Primer #13 for sec
	24	12.2	61.0	38	22	AAH96857	Human Chk1 ribozym
	25	12.2	61.0	47	21	AAZ69349	Human map-related
	26	12	60.0	15	22	AAF69554	Human IL4Ralpha ge
	27	12	60.0	15	22	AAF69556	Human IL4Ralpha ge
c	28	12	60.0	19	21	AAA29708	CC49 heavy chain o
c	29	12	60.0	19	21	AAZ40729	Primer 2 for seque
c	30	12	60.0	19	22	AAS03558	Mouse immunoglobul
c	31	12	60.0	21	22	AAF95584	Human gene single
c	32	12	60.0	22	19	AAV01572	H. capsulatum rRNA
c	33	12	60.0	24	17	AAT06583	Probe A (Set 3) fo
c	34	12	60.0	24	17	AAT06508	Probe A (Set 3) fo
	35	12	60.0	24	20	AAX33219	Human PCP4 gene PC
	36	12	60.0	30	22	AAF76709	PTP Beta coding se
	37	12	60.0	32	20	AAX33195	Human PCP4 gene PC
c	38	12	60.0	35	13	AAQ30765	3F8 VHDJ-human C-g
	39	12	60.0	40	20	AAZ34433	Nucleic acid-based
c	40	12	60.0	42	20	AAX77271	Hexulose phosphate
	41	12	60.0	46	21	AAZ98247	Reductase-thiolase
c	42	12	60.0	50	15	AAQ69506	Human prepro-oxyto
c	43	12	60.0	50	15	AAQ69516	Human plasminogen
c	44	12	60.0	50	17	AAT06582	Target sequence IS
c	45	12	60.0	50	17	AAT06507	Target sequence IS

ALIGNMENTS

RESULT 1
AAT37560/c
ID AAT37560 standard; mRNA; 15 BP.
XX
AC AAT37560;
XX
DT 11-NOV-1996 (first entry)
XX
DE Apo(a) mRNA (nt. pos. 362) hammerhead ribozyme target sequence.
XX
KW Enzymatic RNA molecule; cleavage; apolipoprotein (a); apo(a);
KW hammerhead ribozyme; target sequence; diagnosis; treatment;
KW lipoprotein (a); atherosclerosis; myocardial infarction; stroke;
KW restenosis; heart disease; human; ss.
XX
OS Homo sapiens.
XX
PN WO9609392-A1.
XX
PD 28-MAR-1996.
XX
PF 21-SEP-1995; 95WO-US11995.
XX
PR 23-SEP-1994; 94US-0311760.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI McSwiggen J, Newton RS, Ramharack R, Stinchcomb DT;
XX
DR WPI; 1996-188454/19.
XX
PT Enzymatic RNA mols. which cleave apo(a) mRNA - useful in diagnosis
PT and treatment of conditions related to Lp(a) levels, e.g.
PT atherosclerosis, myocardial infarction, and heart diseases

```
XX
PS   Claim 2; Page 18; 37pp; English.
XX
CC   A claimed enzymatic RNA mol. for the cleavage of apolipoprotein (a)
CC   (apo(a)) mRNA, specifically a hammerhead ribozyme, has binding arms
CC   complementary to the present sequence (nucleotide position 362).
CC   The ribozyme blocks to some extent apo(a) expression, and can
CC   therefore be used to diagnose or treat conditions related to
CC   lipoprotein (a) levels, e.g. atherosclerosis, myocardial
CC   infarction, stroke, restenosis and heart disease.
CC   PCR was used to generate a substrate for T7 RNA polymerase
CC   transcription from human apo(a) cDNA clones. Labelled transcripts
CC   were synthesised in vitro to form 2 templates. The oligonucleotides
CC   and labelled transcripts were annealed, RNaseH added and the mixts.
CC   incubated. After a designated time the reactions were stopped, and
CC   RNA sepd. on sequencing polyacrylamide gels. The percentage of
CC   substrate cleaved was determined by autoradiographic
CC   quantification, and the most accessible ribozyme target sites
CC   chosen.
XX
SQ   Sequence 15 BP; 5 A; 5 C; 3 G; 2 U; 0 other;


  Query Match             75.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 tgcgtctgagcattg 17
          |||||||||||||||
Db     15 TGCGTCTGAGCATTG 1


RESULT   2
AAV23052/c
ID   AAV23052 standard; DNA; 20 BP.
XX
AC   AAV23052;
XX
DT   30-JUL-1998  (first entry)
XX
DE   HG5647S-20 primer used to amplify Hepatitis virus g gene sequences.
XX
KW   Hepatitis g virus gene; diagnosis; treatment; Hepatitis g virus disease;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Hepatitis g virus.
XX
PN   JP10108685-A.
XX
PD   28-APR-1998.
XX
PF   10-AUG-1997;   97JP-0227387.
XX
PR   10-AUG-1996;   96JP-0227639.
XX
PA   (BMLB-) BML KK.
XX
DR   WPI; 1998-304974/27.
XX
PT   New hepatitis G virus gene - useful for diagnosing and treating
PT   diseases caused by virus
XX
PS   Disclosure; Page 6; 128pp; Japanese.
XX
CC   PCR primers AAV23018-74 were used to amplify and isolate new Hepatitis g
CC   virus gene (see AAV23075-83 for gene fragments). RNA was synthesised
CC   from the serum of nine patients judged positive for Hepatitis g virus
CC   and cDNA synthesised from this RNA. The cDNA was used as a template in
CC   several PCR reactions to isolate fragments of the new gene. The gene
CC   may be useful for diagnosing and developing treatments for Hepatitis g
CC   virus diseases.
XX
SQ   Sequence 20 BP; 5 A; 6 C; 8 G; 1 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 19;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 4.6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 gcgtctgagcattgcgt 20
          |||||||||| |||| |
Db     19 GCGTCTGAGCGTTGCCT 3


RESULT   3
AAC70054/c
ID   AAC70054 standard; RNA; 53 BP.
XX
AC   AAC70054;
XX
DT   30-JAN-2001  (first entry)
XX
DE   VEGF-binding nucleic acid ligand identified by SELEX, SEQ ID NO:249.
XX
KW   SELEX; systematic evolution of ligands by exponential enrichment;
KW   nucleic acid ligand; aptamer; in vitro evolution; iterative selection;
KW   human VEGF-binding; vascular endothelial growth factor; ss.
XX
OS   Synthetic.
XX
PN   WO200056930-A1.
XX
PD   28-SEP-2000.
XX
PF   20-MAR-2000; 2000WO-US07486.
XX
PR   24-MAR-1999;   99US-0275850.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
XX
PI   Pagratis N,  Gold L,  Shtatland T,  Javornik B;
XX
DR   WPI; 2000-594583/56.
XX
PT   Identifying nucleic acid ligands of a target molecule comprises
PT   annealing complementary oligonucleotides, partitioning the nucleic
PT   acids and amplifying the nucleic acids exhibiting increased affinity -
XX
PS   Example 9; Page 226; 264pp; English.
XX
CC   The invention relates to a method of identifying nucleic acid ligands of
CC   a target molecule from a candidate mixture composed of single stranded
CC   nucleic acids, each having a region of randomised sequence and a region
CC   of fixed sequence. The method uses modified versions of the SELEX
CC   (systematic evolution of ligands by exponential enrichment) method in
CC   which the participation of fixed sequences is minimised or eliminated.
CC   This method comprises annealing complementary oligonucleotides to the
CC   fixed sequences of the candidate molecule mixture, contacting the
CC   candidate mixture with the target molecule, partitioning the nucleic
CC   acids which have increased affinity relative to the candidate mixture,
CC   and amplifying the nucleic acids exhibiting increased affinity to yield
CC   a ligand enriched mixture of nucleic acids. In one embodiment of the
CC   invention, one or more regions of fixed sequences is replaced with
CC   different fixed sequences, and the binding, partitioning and
CC   amplification steps are repeated. In another embodiment, the partitioned
CC   nucleic acids are hybridised with a library of single stranded
CC   complementary nucleic acids, are then amplified, and the fixed regions
CC   of the increased affinity nucleic acids cleaved. The present sequence
CC   represents a nucleic acid ligand capable of binding to human VEGF
CC   (vascular endothelial growth factor) which was identified using a SELEX
CC   method of the invention.
XX
SQ   Sequence 53 BP; 11 A; 12 C; 18 G; 12 U; 0 other;
```

```
  Query Match            67.0%;  Score 13.4;  DB 21;  Length 53;
  Best Local Similarity  93.3%;  Pred. No. 8.2e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 cgtctgagcattgcg 19
           ||||||||||| |||
Db      43 CGTCTGAGCATAGCG 29


RESULT   4
AAV64594/c
ID   AAV64594 standard; DNA; 28 BP.
XX
AC   AAV64594;
XX
DT   29-JAN-1999  (first entry)
XX
DE   Human native interferon-beta primer F15/C17.
XX
KW   Interferon-Beta; variant; human; medicament; treatment; screening;
KW   multiple sclerosis; measurement; water soluble; primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   DE19717864-A1.
XX
PD   29-OCT-1998.
XX
PF   23-APR-1997;   97DE-1017864.
XX
PR   23-APR-1997;   97DE-1017864.
XX
PA   (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX
PI   Otto B,  Schneider-Fresenius C,  Waschuetza G;
XX
DR   WPI; 1998-569784/49.
XX
PT   New mutated recombinant human interferon-beta protein contains
PT   hydroxylic amino acid substitutions to improve water solubility -
PT   used e.g. in in vitro screening assays, to measure interferon levels
PT   and to treat multiple sclerosis
XX
PS   Disclosure; Fig 4; 18pp; German.
XX
CC   AAV64592-V64610 are primers used in the construction of a mutant human
CC   recombinant interferon-beta in which an amino acid having at least one
CC   hydroxy group is substituted for at least one of Leu5, Phe8, Phe15,
CC   Leu47, Phe50, Leu106, Phe111, Leu116, Leu120 and Phe156. Such mutants
CC   can be used in medicaments e.g. for treating multiple sclerosis, for in
CC   vitro screening assays and for measurement of interferon levels. The
CC   mutated protein is more water-soluble than recombinant wild-type human
CC   interferon-beta.
XX
SQ   Sequence 28 BP; 8 A; 10 C; 5 G; 5 T; 0 other;


  Query Match            66.0%;  Score 13.2;  DB 19;  Length 28;
  Best Local Similarity  83.3%;  Pred. No. 9.6e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 tctgcgtctgagcattgc 18
           |||| | ||||| |||||
Db      22 TCTGGGACTGAGAATTGC 5


RESULT   5
AAA77044
ID   AAA77044 standard; cDNA; 51 BP.
XX
AC   AAA77044;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Human clone cg43328092 polymorphic site, SEQ ID NO:727.
XX
KW   Human; single nucleotide polymorphism; SNP; chromosome 8;
KW   detection; identification; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace (26,G)
FT                   /*tag= a
XX
PN   WO200029623-A2.
XX
PD   25-MAY-2000.
XX
PF   17-NOV-1999;   99WO-US27293.
XX
PR   17-NOV-1998;   98US-0109024.
PR   16-NOV-1999;   99US-0109024.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach MD;
XX
DR   WPI; 2000-387826/33.
XX
PT   Human nucleic acids containing single nucleotide polymorphisms, useful
PT   for treating a subject suffering, or at risk from a pathology due to
PT   the presence of a sequence polymorphism -
XX
PS   Claim 1; Page 377; 543pp; English.
XX
CC   Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC   which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC   1112 (AAA76318-A77429) are consecutive pairs of nucleotides which
CC   contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
CC   consecutive pairs of nucleotides containing SNPs which result in changes
CC   in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC   sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC   changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC   in non- conservative changes. The SNPs in sequences 1187 to 1192
CC   (AAA77504-A77509) generate frameshift mutations. The invention also
CC   relates to a method of detecting a polymorphic site in a nucleic acid and
CC   a method of determining the relatedness of two nucleic acids. It also
CC   encompasses peptides containing polymorphic sites, antibodies raised
CC   against such peptides, and a method of detecting polymorphic
CC   proteins/peptides using the antibodies. The nucleic acids are useful for
CC   gene therapy of an individual having, suspected of having, or at risk of
CC   developing a pathological condition due to the presence of a sequence
CC   polymorphism. Such treatment would comprise administration of the
CC   wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC   peptides can also be used in the treatment of such individuals.
XX
SQ   Sequence 51 BP; 12 A; 10 C; 14 G; 15 T; 0 other;


  Query Match            65.0%;  Score 13;  DB 21;  Length 51;
  Best Local Similarity  100.0%;  Pred. No. 1.3e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tctgcgtctgagc 13
           |||||||||||||
Db      39 tctgcgtctgagc 51


RESULT   6
AAA77045
ID   AAA77045 standard; cDNA; 51 BP.
XX
AC   AAA77045;
XX
```

DT 16-NOV-2000 (first entry)
XX
DE Human clone cg43328092 polymorphic site, SEQ ID NO:728.
XX
KW Human; single nucleotide polymorphism; SNP; chromosome 8;
KW detection; identification; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace (26,A)
FT /*tag= a
XX
PN WO200029623-A2.
XX
PD 25-MAY-2000.
XX
PF 17-NOV-1999; 99WO-US27293.
XX
PR 17-NOV-1998; 98US-0109024.
PR 16-NOV-1999; 99US-0109024.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2000-387826/33.
XX
PT Human nucleic acids containing single nucleotide polymorphisms, useful
PT for treating a subject suffering, or at risk from a pathology due to
PT the presence of a sequence polymorphism -
XX
PS Claim 1; Page 377; 543pp; English.
XX
CC Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC 1112 (AAA76318-A77429) are consecutive pairs of nucleotides which
CC contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
CC consecutive pairs of nucleotides containing SNPs which result in changes
CC in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC in non- conservative changes. The SNPs in sequences 1187 to 1192
CC (AAA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals.
XX
SQ Sequence 51 BP; 11 A; 10 C; 15 G; 15 T; 0 other;

Query Match 65.0%; Score 13; DB 21; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctgcgtctgagc 13
||||||||||||
Db 39 tctgcgtctgagc 51

RESULT 7
AAH45651
ID AAH45651 standard; DNA; 26 BP.
XX
AC AAH45651;
XX
DT 24-SEP-2001 (first entry)
XX
DE PCR primer specific for chondromodulin related cDNA.
XX
KW Transcription factor; chondromodulin-I; chronic rheumatoid arthritis;
KW osteoarthritis; osteoporosis; broken bone; cancer; vertebral disk hernia;
KW sciatica; ectopic chondrogenesis; mouse; PCR primer; ss.
XX
OS Mus sp.
XX
PN WO200138392-A1.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-JP08257.
XX
PR 26-NOV-1999; 99JP-0336475.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Yoshimura K, Hikichi Y, Noguchi K;
XX
DR WPI; 2001-355908/37.
XX
PT Polypeptides for treatment and prevention of chronic rheumatoid
PT arthritis, osteoarthritis, osteoporosis, broken bones, cancer,
PT vertebral disk hernia, sciatica and ectopic chondrogenesis -
XX
PS Example 3; Page 92; 99pp; Japanese.
XX
CC This invention relates to a transcription factor polypeptide sequence,
CC and the DNA encoding it. Included in the invention are vectors containing
CC the DNA, hosts transformed by the vectors, and antibodies directed
CC against the proteins. A drug containing compounds which affect the action
CC of the proteins is used for the treatment and prevention of chronic
CC rheumatoid arthritis, osteoarthritis, osteoporosis, broken bones, cancer,
CC vertebral disk hernia, sciatica and ectopic chondrogenesis. The present
CC sequence represents a PCR primer specific for cDNA related to murine
CC chondromodulin, the transcription factor of the invention, binds to the
CC promoter of the chondromodulin-I gene.
XX
SQ Sequence 26 BP; 3 A; 6 C; 9 G; 8 T; 0 other;

Query Match 64.0%; Score 12.8; DB 22; Length 26;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 cgtctgagcattgcgt 20
||||||| ||||| ||
Db 7 cgtctgaacattgggt 22

RESULT 8
AAX92916
ID AAX92916 standard; DNA; 20 BP.
XX
AC AAX92916;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydia pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.

XX
PF 20-NOV-1998; 98WO-IB01890.
XX
PR 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae
XX
PS Page 1549; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading
CC frames and other nucleic acid sequences from the genome of
CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
CC disease such as pneumonia and bronchitis and is thought to be a
CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC by the open reading frames of the C. pneumoniae genome (see AAY34584-
CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC containing C. pneumoniae nucleotides sequences can also be used as
CC immunogenic compositions, especially where the vector directs the
CC expression of a neutralising epitope of C. pneumoniae.
XX
SQ Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 other;

Query Match 63.0%; Score 12.6; DB 20; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tctgcgtctgagcattgcg 19
| ||| ||||| | |||||
Db 2 tatgcctctgatccttgcg 20

RESULT 9
AAA35410/c
ID AAA35410 standard; DNA; 22 BP.
XX
AC AAA35410;
XX
DT 25-JUL-2000 (first entry)
XX
DE Myrtaceae microsatellite scu048TT detection PCR primer.
XX
KW Myrtaceae; microsatellite; isolation; genotyping; plant; tea tree;
KW breeding; Melaleuca alternifolia; broad-spectrum germicidal oil;
KW pharmaceutical; cosmetic; identification; detection; PCR primer; ss.
XX
OS Myrtaceae sp.
XX
PN WO200017341-A1.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-AU00820.
XX
PR 23-SEP-1998; 98AU-0006099.
PR 16-FEB-1999; 99AU-0008718.
XX
PA (BUSI-) BUSINESS & RES MANAGEMENT PTY LTD.
XX
PI Rossetto M, McLauchlan A, Harriss FCL, Henry RJ, Baverstock PR;
PI Lee LS, Maguire TL, Edwards KJ;
XX
DR WPI; 2000-292840/25.
XX
PT Isolating microsatellites from Myrtaceae, useful for genotyping,
PT particularly in breeding programs for tea tree, by reacting plant
PT nucleic acid with immobilized oligonucleotides -
XX
PS Claim 10; Page 36; 100pp; English.
XX
CC A method has been developed of isolating a microsatellite (MS) from
CC nucleic acid extract of a plant of Myrtaceae family. The method
CC comprises: (i) treating the extract with one or more immobilised,
CC single-stranded oligonucleotides (ON) having a consensus MS repeat
CC sequence (MSRS) or its complement; (ii) washing under specified
CC stringency conditions; (iii) eluting nucleic acid bound to ON; and
CC (iv) sequencing the eluted nucleic acids to identify those containing
CC an MSRS. Microsatellites (MS) isolated by the method, specifically
CC from Melaleuca alternifolia (the tea tree, a source of a broad-spectrum
CC germicidal oil, useful in pharmaceuticals and cosmetics), are useful as
CC genotyping markers, particularly for breeding plants that produce the
CC oil in higher yield or of better quality. Primers based on MS are
CC useful for both inter- and intra-species genotyping. The selected
CC washing conditions improve efficiency of recovery of microsatellites
CC (MS) and reduce the number of washing stages required. Particularly
CC about 86% of recovered sequence contain an MS repeat sequence,
CC compared with 50-70% when the conventional washing procedure is
CC followed. AAA35313 to AAA35357, and AAA35562 to AAA35575 represent
CC nucleotide sequences from the present invention which contain
CC microsatellite sequences. AAA35358 to AAA35561 represent oligonucleotide
CC PCR primers used for identifying Myrtaceae microsatellite sequences.
XX
SQ Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 other;

Query Match 63.0%; Score 12.6; DB 21; Length 22;
Best Local Similarity 78.9%; Pred. No. 1.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ctgcgtctgagcattgcgt 20
||| | ||| |||||||
Db 21 CTGAGACTGTGCATTGCCT 3

RESULT 10
AAT30288/c
ID AAT30288 standard; DNA; 25 BP.
XX
AC AAT30288;
XX
DT 29-NOV-1996 (first entry)
XX
DE Nuclear polyhedrosis virus polyhedrin gene detection primer 4.
XX
KW Primer; PCR; amplification; polymerase chain reaction; insect; shellfish;
KW nuclear polyhedrosis virus; polyhedrin; p10; Autographa californica;
KW Bombyx mori; Perina nuda; Spodoptera frugiperda; detection; ss.
XX
OS Synthetic.
XX
PN US5521299-A.
XX
PD 28-MAY-1996.
XX
PF 22-NOV-1994; 94US-0343379.
XX
PR 22-NOV-1994; 94US-0343379.
XX
PA (NASC-) NAT SCI COUNCIL.
XX
PI Chou C, Huang C, Kou G, Lo C, Wang C;
XX
DR WPI; 1996-267861/27.
XX
PT Primer mixt. specific for nuclear polyhedrosis virus - used in PCR
PT detection of infection in insects and shellfish
XX
PS Disclosure; Column 2; 8pp; English.

```
XX
CC   The primers AAT30277-90 are used in a method to detect nuclear
CC   polyhedrosis viruses (NPV) in insects and shellfish.  The primers
CC   AAT30277-8 amplify a 160 bp fragment of the polyhedrin gene, whereas the
CC   primer sets AAT30279-82 and AAT30283-6 amplify a 680 bp fragment of the
CC   p10 gene from these viruses.  The amplified fragment sizes are conserved
CC   across a range of NPVs e.g. Autographa californica NPV, Bombyx mori NPV,
CC   Perina nuda NPV, Spodoptera frugiperda NPV, etc.  The primers allow esp.
CC   rapid detection of these viruses which can cause severe losses amongst
CC   commercially important shellfish. These primers are specific examples of
CC   the set 1 primer AAT30277.
XX
SQ   Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 other;


  Query Match             63.0%;  Score 12.6;  DB 17;  Length 25;
  Best Local Similarity   78.9%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 ctgcgtctgagcattgcgt 20
           | |||||| ||  ||||||
Db      24 CGGCGTCTAAGATTTGCGT 6


RESULT  11
AAT59325/c
ID   AAT59325 standard; DNA; 25 BP.
XX
AC   AAT59325;
XX
DT   22-APR-1997  (first entry)
XX
DE   DNA primer for Baculovirus screening.
XX
KW   primer; polymerase chain reaction; PCR; detection; Baculovirus;
KW   nuclear polyhedrosis virus; Autographica californica; Bombyx mori;
KW   Perina nuda; AcNPV; BmNPV; PnNPV; polyhedrin; p10 gene; ss.
XX
OS   Synthetic.
XX
PN   JP08308600-A.
XX
PD   26-NOV-1996.
XX
PF   05-JAN-1995;   95JP-0016515.
XX
PR   05-JAN-1995;   95JP-0016515.
XX
PA   (NASC-) NAT SCI COUNCIL.
XX
DR   WPI; 1997-059712/06.
XX
PT   Oligo:nucleotide primer mixtures for detection of Baculovirus
PT   infection - provides simple and rapid means of detection
XX
PS   Example 1; Page 7; 9pp; Japanese.
XX
CC   AAT59324-27 are primers disclosed in an example of the method of the
CC   invention.  They are used for the detection of Baculovirus infection in
CC   a sample. PCR amplification of the p10 gene was used for detection of
CC   AcPNV and PnNPV, and the polyhedrin gene was used for detection of AcPNV
CC   and BmNPV. The primers provide simple and rapid means of detection.
XX
SQ   Sequence 25 BP; 6 A; 6 C; 5 G; 8 T; 0 other;


  Query Match             63.0%;  Score 12.6;  DB 18;  Length 25;
  Best Local Similarity   78.9%;  Pred. No. 1.9e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 ctgcgtctgagcattgcgt 20
           | |||||| ||  ||||||
Db      24 CGGCGTCTAAGATTTGCGT 6


RESULT  12
AAI30310/c
ID   AAI30310 standard; DNA; 31 BP.
XX
AC   AAI30310;
XX
DT   18-OCT-2001  (first entry)
XX
DE   Human single nucleotide polymorphism (SNP) LTB 2.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(16,A)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200166800-A2.
XX
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US07268.
XX
PR   07-MAR-2000; 2000US-0187510.
PR   22-MAY-2000; 2000US-0206129.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or
PT   severity of a particular phenotype or disorder (e.g. diabetes)
PT   associated with a particular genotype -
XX
PS   Claim 1; Page 78; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing.
XX
SQ   Sequence 31 BP; 3 A; 10 C; 13 G; 5 T; 0 other;


  Query Match             63.0%;  Score 12.6;  DB 22;  Length 31;
  Best Local Similarity   78.9%;  Pred. No. 2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 tctgcgtctgagcattgcg 19
           || ||||| ||| | ||||
Db      19 TCGGCGTCCGAGAACTGCG 1


RESULT  13
AAH89265/c
ID   AAH89265 standard; DNA; 51 BP.
XX
AC   AAH89265;
XX
DT   01-OCT-2001  (first entry)
```

XX
DE Human coding sequence polymorphic site SEQ ID NO: 46.
XX
KW Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
XX
OS Homo sapiens.
XX
PN WO200151670-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US00322.
XX
PR 07-JAN-2000; 2000US-0174962.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2001-451871/48.
DR P-PSDB; AAM00156.
XX
PT Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes -
XX
PS Claim 1; Page 122; 475pp; English.
XX
CC The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tuberous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention.
XX
SQ Sequence 51 BP; 11 A; 11 C; 13 G; 16 T; 0 other;

Query Match 63.0%; Score 12.6; DB 22; Length 51;
Best Local Similarity 78.9%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 tctgcgtctgagcattgcg 19
||||||| |||| | || |
Db 30 TCTGCGTGTGAGAACTGTG 12

RESULT 14
AAQ32826
ID AAQ32826 standard; DNA; 20 BP.
XX
AC AAQ32826;
XX
DT 05-MAY-1993 (first entry)
XX
DE Microsatellite repeat polymorphic DNA marker PCR primer.
XX
KW PIC; high polymorphism information content; forensic; screening;
KW polymerase chain reaction; genetic mapping; paternity; prenatal.
XX
OS Synthetic.
XX
PN WO9221693-A.
XX
PD 10-DEC-1992.
XX
PF 27-MAY-1992; 92WO-US04195.
XX
PR 29-MAY-1991; 91US-0707501.
PR 27-NOV-1991; 91US-0799828.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX
PI Merrill CR, Polymeropoulos MH;
XX
DR WPI; 1992-433606/52.
XX
PT Oligo-nucleotide primers for polymerase chain reaction
PT amplification - which detect DNA polymorphisms and are useful for
PT prenatal and paternity screening, and genetic mapping
XX
PS Disclosure; Fig 46; 44pp; English.
XX
CC This is a PCR primer which is used (with AAQ32827) to characterise
CC a unique microsatellite repeat polymorphic DNA marker which has a
CC high polymorphism information content. The marker is useful for
CC human individualisation, in forensic screening, in paternity and
CC prenatal screening as well as in genetic mapping.
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;

Query Match 62.0%; Score 12.4; DB 13; Length 20;
Best Local Similarity 92.9%; Pred. No. 2.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ctgcgtctgagcat 15
|||| |||||||||
Db 1 ctgcatctgagcat 14

RESULT 15
AAQ57849
ID AAQ57849 standard; DNA; 20 BP.
XX
AC AAQ57849;
XX
DT 21-AUG-1994 (first entry)
XX
DE Primer pair 19A HSMYH01 detection primer #1.
XX
KW Primer; assay; subtle difference; dinucleotide; tetranucleotide;
KW repeat; polymorphism; PCR; polymerase chain reaction; amplify; PAGE;
KW autoradiography; migration pattern; length variation; genetic mapping;
KW forensic screening; paternity; prenatal; screening; microsatellite;
KW human; ss.
XX
OS Synthetic.
XX
PN WO9403640-A.
XX
PD 17-FEB-1994.
XX
PF 30-JUL-1993; 93WO-US07183.
XX
PR 31-JUL-1992; 92US-0922723.
PR 28-SEP-1992; 92US-0952277.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Merril CR, Polymeropolous MH;
XX
DR WPI; 1994-065727/08.
XX
PT New polynucleotide sequences - derived from polymorphic
PT micro:satellite repeats, used for characterising human
PT individuals for forensic, paternity and prenatal screening and
PT genetic mapping
XX
PS Disclosure; Page 43; 72pp; English.

XX
CC The sequences given in AAQ57782-866 are primers which were used in
CC an assay for measuring the subtle differences in genetic material
CC regarding an added or omitted set of dinucleotide or tetranucleotide
CC repeat polymorphisms. The method comprises obtaining polynucleotide
CC segments comprising the repeat polymorphisms in an amount effective
CC for testing and amplifying the segments by a PCR procedure using a
CC pair of oligonucleotide primers capable of amplifying the polymorphism
CC containing sequence. The amplified sequences are resolved using PAGE
CC and the resolved sequences are compared by autoradiography to observe
CC the differences in migration pattern due to length variation. The
CC polynucleotides provide a fast and accurate test for measuring the
CC subtle differences in individuals in eg. forensic screening, paternity
CC and prenatal screening and genetic mapping. The polynucleotides are
CC specific for polymorphic microsatellite repeats based on previously
CC sequenced human genes.
XX
SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;

Query Match 62.0%; Score 12.4; DB 15; Length 20;
Best Local Similarity 92.9%; Pred. No. 2.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ctgcgtctgagcat 15
|||| |||||||||
Db 1 ctgcatctgagcat 14

Search completed: March 13, 2002, 09:50:20
Job time: 5129 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 10:55:21 ; Search time 968.42 Seconds
(without alignments)
17.706 Million cell updates/sec

Title: US-09-923-515-39
Perfect score: 20
Sequence: 1 accttaaaagcttatacaca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	15	75.0	15	17	AAT37625	Apo(a) mRNA (nt. p
c	2	14.4	72.0	42	19	AAV11897	L. lactis NS3 locu
c	3	14.2	71.0	22	14	AAQ46058	Sequence of PCR pr
	4	13.8	69.0	17	21	AAA25744	Oestrogen receptor
	5	13.8	69.0	29	22	AAF58627	Murine N-myc mutan
c	6	13.8	69.0	38	21	AAA07203	PCR primer for eno
c	7	13.8	69.0	38	21	AAZ98264	A. caviae phaJ gen
c	8	13.6	68.0	24	21	AAA38088	Oligonucleotide OD
c	9	13.6	68.0	24	21	AAA14544	Primer ODN-RT(-) w
c	10	13.6	68.0	24	21	AAA14553	Oligonucleotide 3'
c	11	13.6	68.0	24	22	AAS02282	Moloney murine leu
c	12	13.6	68.0	24	22	AAS02674	Oligodeoxynucleoti
c	13	13.6	68.0	29	13	AAQ32017	86Q3 toxin gene re
c	14	13.6	68.0	29	15	AAQ67666	PCR primer for del
c	15	13.6	68.0	29	15	AAQ77696	B. thuringiensis w
c	16	13.6	68.0	29	16	AAQ81167	B.t. toxin PS86Q3
c	17	13.6	68.0	29	16	AAQ81160	B.t. PS80JJ1 toxin
c	18	13.6	68.0	29	16	AAQ91783	B. thuringiensis e
c	19	13.6	68.0	29	18	AAT89183	Primer for coding
c	20	13.6	68.0	29	18	AAT77276	Bacillus thuringie
c	21	13.6	68.0	29	18	AAT66810	Bacillus thuringie
c	22	13.6	68.0	29	18	AAT60055	Probe #7 for ant-a
c	23	13.6	68.0	29	18	AAT61020	B. thuringiensis n
c	24	13.6	68.0	29	19	AAV58997	B.t. toxin gene pr
c	25	13.6	68.0	29	19	AAV15224	Bacillus thuringie
c	26	13.6	68.0	29	21	AAA65107	Probe #10 used to
c	27	13.6	68.0	29	22	AAF28509	Probe #7. Bacillu
c	28	13.6	68.0	29	22	AAA89223	Bacillus thuringie
c	29	13.6	68.0	48	18	AAT60062	Primer #2 for 86Q3
c	30	13.6	68.0	48	19	AAV59004	B.t. toxin gene pr
c	31	13.6	68.0	48	21	AAA65113	Protoxin T 5' prim
c	32	13.6	68.0	51	22	AAH89366	Human nuclease cod
c	33	13.6	68.0	51	22	AAH89367	Human nuclease cod
c	34	13.6	68.0	57	19	AAV17727	T1 receptor-like l
c	35	13.4	67.0	40	21	AAA56045	Plasmid pLAC11-rec
	36	13.2	66.0	28	20	AAV71963	Fas ligand (FasL)
	37	13.2	66.0	29	16	AAQ91784	B. thuringiensis e
c	38	13.2	66.0	33	21	AAA14776	PCR primer used to
c	39	13.2	66.0	35	22	AAH38361	SNP specific upper
c	40	13.2	66.0	37	16	AAQ98943	Virgiferin antisen
c	41	13	65.0	22	16	AAQ94227	Bovine Neospora nu
c	42	13	65.0	22	19	AAV00079	Bovine Neospora fo
c	43	13	65.0	22	21	AAA94195	Neospora nss-rRNA
c	44	13	65.0	23	22	AAH03102	Microorganism dete
c	45	13	65.0	30	19	AAV03270	Homo sapiens melan

ALIGNMENTS

RESULT 1
AAT37625/c
ID AAT37625 standard; mRNA; 15 BP.
XX
AC AAT37625;
XX
DT 11-NOV-1996 (first entry)
XX
DE Apo(a) mRNA (nt. pos. 13848) hammerhead ribozyme target sequence.
XX
KW Enzymatic RNA molecule; cleavage; apolipoprotein (a); apo(a);
KW hammerhead ribozyme; target sequence; diagnosis; treatment;
KW lipoprotein (a); atherosclerosis; myocardial infarction; stroke;
KW restenosis; heart disease; human; ss.
XX
OS Homo sapiens.
XX
PN WO9609392-A1.
XX
PD 28-MAR-1996.
XX
PF 21-SEP-1995; 95WO-US11995.
XX
PR 23-SEP-1994; 94US-0311760.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI McSwiggen J, Newton RS, Ramharack R, Stinchcomb DT;
XX
DR WPI; 1996-188454/19.
XX
PT Enzymatic RNA mols. which cleave apo(a) mRNA - useful in diagnosis
PT and treatment of conditions related to Lp(a) levels, e.g.
PT atherosclerosis, myocardial infarction, and heart diseases

```
XX
PS   Claim 2; Page 18; 37pp; English.
XX
CC   A claimed enzymatic RNA mol. for the cleavage of apolipoprotein (a)
CC   (apo(a)) mRNA, specifically a hammerhead ribozyme, has binding arms
CC   complementary to the present sequence (nucleotide position 13848).
CC   The ribozyme blocks to some extent apo(a) expression, and can
CC   therefore be used to diagnose or treat conditions related to
CC   lipoprotein (a) levels, e.g. atherosclerosis, myocardial
CC   infarction, stroke, restenosis and heart disease.
CC   PCR was used to generate a substrate for T7 RNA polymerase
CC   transcription from human apo(a) cDNA clones. Labelled transcripts
CC   were synthesised in vitro to form 2 templates. The oligonucleotides
CC   and labelled transcripts were annealed, RNaseH added and the mixts.
CC   incubated. After a designated time the reactions were stopped, and
CC   RNA sepd. on sequencing polyacrylamide gels. The percentage of
CC   substrate cleaved was determined by autoradiographic
CC   quantification, and the most accessible ribozyme target sites
CC   chosen.
XX
SQ   Sequence 15 BP; 3 A; 1 C; 3 G; 8 U; 0 other;


  Query Match            75.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 aaaagcttatacaca 20
          ||||||||||||||||
Db     15 AAAAGCTTATACACA 1


RESULT   2
AAV11897/c
ID   AAV11897 standard; DNA; 42 BP.
XX
AC   AAV11897;
XX
DT   13-AUG-1998  (first entry)
XX
DE   L. lactis NS3 locus PCR primer NS3-8.
XX
KW   Salt-inducible promoter; lactic acid; food industry; food-grade inducer;
KW   fermentation processes; cheese production; PCR primer; ss.
XX
OS   Synthetic.
OS   Lactococcus lactis.
XX
PN   WO9810080-A1.
XX
PD   12-MAR-1998.
XX
PF   20-AUG-1997;   97WO-EP04755.
XX
PR   13-MAR-1997;   97EP-0200744.
PR   05-SEP-1996;   96EP-0202444.
XX
PA   (UNIL ) UNILEVER NV.
PA   (UNIL ) UNILEVER PLC.
XX
PI   Kok J,  Ledeboer AM,  Sanders JW,  Venema G;
XX
DR   WPI; 1998-193629/17.
XX
PT   Salt-inducible promoter - derived from lactic acid bacteria, used
PT   for the production of polypeptides in food
XX
PS   Disclosure; Page 16; 111pp; English.
XX
CC   AAV11892-V11900 are PCR primers used in the identification and isolation
CC   of a salt-inducible promoter (SIP) derived from the lactic acid
CC   bacterium Lactococcus lactis. Using the SIP, salt can be used as a
CC   food-grade inducer in food fermentation processes, e.g. in the
CC   production of cheese, dressings, water-containing spreads, sausages,
CC   or sour dough.
XX
SQ   Sequence 42 BP; 8 A; 8 C; 10 G; 16 T; 0 other;


  Query Match            72.0%;  Score 14.4;  DB 19;  Length 42;
  Best Local Similarity  93.8%;  Pred. No. 6.4e+02;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 cttaaaagcttataca 18
          | ||||||||||||||
Db     36 CATAAAAGCTTATACA 21


RESULT   3
AAQ46058/c
ID   AAQ46058 standard; DNA; 22 BP.
XX
AC   AAQ46058;
XX
DT   08-FEB-1994  (first entry)
XX
DE   Sequence of PCR primer L03 for the amplification of hly virulence
DE   factor.
XX
KW   Virulence factor; Listeria detection; food poisoning; hly; PCR;
KW   primer; ss.
XX
OS   Synthetic.
XX
PN   CH682156-A.
XX
PD   30-JUL-1993.
XX
PF   28-JUN-1990;   90CH-0002190.
XX
PR   28-JUN-1990;   90CH-0002190.
XX
PA   (CAND/) CANDRIAN U.
PA   (FURR/) FURRER B.
PA   (HOEF/) HOEFELEIN C.
PA   (LUET/) LUETHY J.
XX
PI   Candrian U,  Furrer B,  Hoefelein C,  Luethy J;
XX
DR   WPI; 1993-265174/34.
XX
PT   Listeria monocytogenes detection by enzymatic nucleic acid
PT   amplification - using oligo-nucleotide(s) derived from
PT   alpha-haemolysin and/or beta-haemo-lysin virulence factors in
PT   polymerase chain reactions
XX
PS   Claim 2; Page 2; 2pp; German.
XX
CC   Oligos L01, L02, L03 and L04 are used for the amplification of hly
CC   (alphy-haemolysin) virulence factor; and oligos AD07, AD08 and AD09
CC   are used for the amplification of iap (beta-haemolysin) virulence
CC   factor. They are used in a detection method for Listeria
CC   monocytogenes in food samples which is faster and more sensitive
CC   than the classical bacteriological methods.
XX
SQ   Sequence 22 BP; 6 A; 4 C; 4 G; 8 T; 0 other;


  Query Match            71.0%;  Score 14.2;  DB 14;  Length 22;
  Best Local Similarity  84.2%;  Pred. No. 7.7e+02;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 ccttaaaagcttatacaca 20
          | | ||||||||||||| |
Db     22 CTTCAAAAGCTTATACAGA 4
```

```
RESULT   4
AAA25744
ID   AAA25744 standard; DNA; 17 BP.
XX
AC   AAA25744;
XX
DT   19-JUL-2000  (first entry)
XX
DE   Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2242.
XX
KW   Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW   hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW   gene expression modification; cancer; phosphorothioate; endonuclease;
KW   anticancer; breast cancer; endometrium cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954459-A2.
XX
PD   28-OCT-1999.
XX
PF   19-APR-1999;   99WO-US08547.
XX
PR   20-APR-1998;   98US-0082404.
PR   23-JUN-1998;   98US-0103636.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Beigelman L,  McSwiggen JA,  Karpeisky A,  Bellon L;
PI   Reynolds M,  Zwick M,  Jarvis T,  Woolf T,  Haeberli P;
PI   Matulic-Adamic J;
XX
DR   WPI; 2000-013248/01.
XX
PT   New nucleic acids that interact, and optionally cleave, target
PT   sequences, used to treat cancer  -
XX
PS   Claim 77; Page 89; 148pp; English.
XX
CC   The present invention describes nucleic acids (A) that interact stably
CC   with a target sequence and contain at least one phosphoro(di)thioate
CC   link, having endonuclease activity. (A), and more generally any
CC   catalytic nucleic acid (A') that modulates expression of the oestrogen
CC   receptor gene, are used to treat cancer (particularly of breast or
CC   endometrium), in vivo or by transforming cells ex vivo and implanting
CC   treated cells, or for other conditions associated with levels of
CC   oestrogen receptor. Because of the high selectivity for targeted RNA, (A)
CC   can also be used to correlate inhibition of gene expression with
CC   alterations in phenotype, particularly for identification of therapeutic
CC   targets, and as research reagents (for RNA, in the  same way that
CC   restriction endonucleases are used with DNA). The combination of
CC   modifications in (A) improves resistance to nucleases, binding affinity
CC   and/or activity. AAA23503 to AAA24747 represent oestrogen receptor
CC   hammerhead ribozyme sequences, and AAA24748 to AAA25992 represent their
CC   corresponding target sequences. AAA25993 to AAA26105 represent oestrogen
CC   receptor hairpin ribozyme sequences, and AAA26107 to AAA26218 represent
CC   their corresponding target sequences. AAA26219 to AAA26271 represent
CC   other ribozyme sequences and antisense oligonucleotides used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 17 BP; 6 A; 4 C; 1 G; 6 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 21;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 cttaaaagcttatacac 19
          ||| ||| |||||||||
Db      1 cttgaaatcttatacac 17
```

```
RESULT   5
AAF58627
ID   AAF58627 standard; DNA; 29 BP.
XX
AC   AAF58627;
XX
DT   27-APR-2001  (first entry)
XX
DE   Murine N-myc mutant oligonucleotide.
XX
KW   Mouse; N-myc; drosophila recombination associated protein; DRAP;
KW   gene targeting; RFLP; restriction fragment length polymorphism; ss.
XX
OS   Mus sp.
XX
PN   WO200107627-A1.
XX
PD   01-FEB-2001.
XX
PF   21-JUL-2000; 2000WO-US19901.
XX
PR   21-JUL-1999;   99US-0144736.
XX
PA   (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI   Eisen A;
XX
DR   WPI; 2001-168555/17.
XX
PT   New nucleic acid encoding Drosophila Recombination-Associated Protein
PT   is useful for genomic cloning, gene isolation and gene mapping  -
XX
PS   Example 7; Page 40; 63pp; English.
XX
CC   The present sequence was used in an example outlined in a specification
CC   relating to an isolated nucleic acid encoding Drosophila
CC   Recombination-Associated Protein (DRAP). DRAP is useful for isolating
CC   genomic DNA, targeting mutagenesis of a defined segment of DNA, removing
CC   a segment of DNA, cloning a defined segment of DNA, mapping a defined
CC   segment of DNA, promoting gene disruptions of a defined segment of DNA,
CC   and experimental and therapeutic application of DRAP driven genetic
CC   modification of a gene responsible for a genetic disease.
CC   The DRAP gene is suitable for very efficient gene targeting.
XX
SQ   Sequence 29 BP; 9 A; 8 C; 4 G; 8 T; 0 other;


  Query Match             69.0%;  Score 13.8;  DB 22;  Length 29;
  Best Local Similarity   88.2%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 ccttaaaagcttataca 18
          ||| |||||||||| ||
Db      4 cctgaaaagcttattca 20
```

```
RESULT   6
AAA07203/c
ID   AAA07203 standard; DNA; 38 BP.
XX
AC   AAA07203;
XX
DT   22-JUN-2000  (first entry)
XX
DE   PCR primer for enoyl-CoA hydratase gene.
XX
KW   PCR primer; polyhydroxyalkanoate synthesis; thiolate; reductase;
KW   poly-3-hydroxyalkanoate; PHA synthase; poly-3-hydroxybutyrate;
KW   PHB synthase; acyl-coenzyme A transferase; enoyl-coenzyme A hydratase;
KW   biological polyester; biodegradable material;
KW   biocompatible thermoplastic material; ss.
XX
OS   Aeromonas caviae.
```

XX
PN WO200011188-A1.
XX
PD 02-MAR-2000.
XX
PF 17-AUG-1999; 99WO-US18673.
XX
PR 18-AUG-1998; 98US-0096852.
XX
PA (META-) METABOLIX INC.
XX
PI Huisman GW, Peoples OP, Skraly F;
XX
DR WPI; 2000-224705/19.
XX
PT Genetically engineered microorganisms for production of
PT polyhydroxyalkanoates for use in industrial and biomedical applications
PT -
XX
PS Example 12; Page 34; 54pp; English.
XX
CC This sequence is a PCR primer for the A. caviae enoyl-CoA hydratase
CC gene. The invention relates to a genetically engineered microorganism
CC having at least one gene involved in synthesis of polyhydroxyalkanoates
CC (selected from thiolate, reductase, poly(3-hydroxyalkanoates) (PHA)
CC synthase, poly-3-hydroxybutyrate (PHB) synthase, acyl-coenzyme A
CC transferase, and enoyl-coenzyme A hydratase), integrated into the
CC chromosome. The microorganisms can be used in methods for screening for
CC genes involved in polyhydroxyalkanoate synthesis, and for production of
CC polyhydroxyalkanoates. The genetically engineered microorganisms and
CC methods are useful for the synthesis and production of
CC polyhydroxyalkanoates, biological polyesters which are biodegradable and
CC biocompatible thermoplastic materials, having industrial and biomedical
CC applications. The microbial strains are advantageous in
CC polyhydroxyalkanoates productions because no plasmids need to be
CC maintained, generally obviating the required use of antibiotics or other
CC stabilising pressures, and no plasmid loss occurs, stabilising the number
CC of gene copies per cell throughout the fermentation process, resulting in
CC homogeneous polyhydroxyalkanoate product formation.
XX
SQ Sequence 38 BP; 8 A; 11 C; 9 G; 10 T; 0 other;

Query Match 69.0%; Score 13.8; DB 21; Length 38;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ccttaaaagcttataca 18
||||||||||||| || |
Db 19 CCTTAAAAGCTTCTAGA 3

RESULT 7
AAZ98264/c
ID AAZ98264 standard; DNA; 38 BP.
XX
AC AAZ98264;
XX
DT 05-JUN-2000 (first entry)
XX
DE A. caviae phaJ gene amplifying primer J12 dw II.
XX
KW Biosynthetic enzyme; fusion protein; beta-ketothiolase; PHA synthase;
KW acyl-CoA reductase; PHB synthetase; polyhydroxybutarate synthetase;
KW enoyl-CoA hydratase; beta-hydroxyacyl-ACP::coenzyme-A transferase;
KW phasin; phaJ gene; PCR primer; ss.
XX
OS Aeromonas caviae.
XX
PN WO200006747-A2.
XX
PD 10-FEB-2000.
XX
PF 30-JUL-1999; 99WO-US17452.
XX
PR 30-JUL-1998; 98US-0094674.
XX
PA (META-) METABOLIX INC.
XX
PI Peoples OP, Madison L, Huisman GW;
XX
DR WPI; 2000-195306/17.
XX
PT New enzymatic fusion proteins useful for producing
PT polyhydroxyalkanoates in seeds of transgenic plants such as sunflower,
PT soybean, and in bacteria, comprises enzymes involved in
PT polyhydroxyalkanoates biosynthesis -
XX
PS Example 4; Page 27; 35pp; English.
XX
CC The invention provides fusion proteins that comprise a heterodimer of
CC poly((R)-3-hydroxyalkanoate) (PHA) biosynthetic enzymes fused through a
CC linker. The fusion proteins are of the formula: E1-L_n-E2 E2-L_n-E1
CC E1 and E2 = beta-ketothiolases, acyl-CoA reductases, PHA synthases, PHB
CC (polyhydroxybutarate) synthetases, phasins, enoyl-CoA hydratases and
CC beta-hydroxyacyl-ACP::coenzyme-A transferase; L_n = a peptide of n amino
CC acids that links E1 to E2 or E2 to E1. Genetically engineered bacterial
CC and plant systems are useful for enhanced production of PHAs in them.
CC The fusion proteins can be expressed in transgenic microbial or plant
CC crop PHA production systems. The fusions can be expressed in the cytosol
CC or subcellular organelles of higher plant such as the seed of an oil
CC crop Brassica, sunflower, soybean, corn, safflower, flax, palm or coconut
CC and starch accumulating plants such as potato, tapioca, cassava, fiber
CC plants such as cotton, hemp or the green tissue of tobacco, alfalfa,
CC switch grass or other forage crops. Use of hybrid enzyme and its
CC corresponding gene is advantageous since combining the two enzyme
CC activities in a single transcriptional unit reduces the number of genes
CC that need to be expressed in transgenic organisms, and the close
CC proximity of two enzyme activities which catalyze sequential steps in a
CC metabolic pathway. The fusion enzyme also allows for direct transfer of
CC the reaction product from the first catalytic domain to the second
CC domain. Sequences AAZ98263-266 represent PCR primers for amplifying the
CC phaJ gene encoding (R)-specific enoyl-CoA transferase from A. caviae.
CC This is used in the construction of PHA synthase-hydratase fusions.
XX
SQ Sequence 38 BP; 8 A; 11 C; 9 G; 10 T; 0 other;

Query Match 69.0%; Score 13.8; DB 21; Length 38;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ccttaaaagcttataca 18
||||||||||||| || |
Db 19 CCTTAAAAGCTTCTAGA 3

RESULT 8
AAA38088/c
ID AAA38088 standard; DNA; 24 BP.
XX
AC AAA38088;
XX
DT 24-AUG-2000 (first entry)
XX
DE Oligonucleotide ODN-RT(-).
XX
KW Single stranded DNA production; gene therapy; gene expression regulator;
KW viral infection; ss.
XX
OS Synthetic.
XX
PN WO200022113-A1.
XX
PD 20-APR-2000.
XX

PF 12-OCT-1999; 99WO-US23933.
XX
PR 09-OCT-1998; 98US-0169793.
PR 16-SEP-1999; 99US-0397783.
XX
PA (INGE-) INGENE INC.
PA (CRYO-) CRYOGENIC SOLUTIONS INC.
XX
PI Skillern MJ, Conrad CA, Elliston JF;
XX
DR WPI; 2000-317973/27.
XX
PT Genetic elements for producing and delivering single stranded cDNA
PT transcripts and inhibitory nucleic acid molecules, comprises sequence
PT of interest and a binding site for reverse transcriptase -
XX
PS Example 1; Page 27; 42pp; English.
XX
CC The present invention relates to a set of genetic elements for delivery
CC into a cell comprising a nucleic acid construct comprising a sequence of
CC interest and a primer binding site for a reverse transcriptase located in
CC a 3' position with respect to the sequence of interest. A vector
CC comprising the set of genetic elements is used in a kit for producing
CC single stranded nucleic acid sequences. The present sequence represents
CC an oligonucleotide used in the construction of plasmids used in the
CC course of the invention. The genetic elements, vectors containing them,
CC and host cells transformed with the vectors are useful for producing and
CC delivering a single stranded nucleic acid sequence of interest
CC particularly a cDNA transcript, an inhibitory molecule, an mRNA
CC transcript and a heteroduplex molecule which involves introducing the
CC genetic elements into a target cell. The process of producing single
CC stranded nucleic acid further comprises a step of removing mRNA from an
CC mRNA/cDNA heteroduplex by RNAse H. The genetic elements, vector, and
CC transformed cells producing inhibitory nucleic acid molecules to a target
CC cell are useful for gene therapy to alleviate pathological conditions
CC such as tumours and viral infections by regulating gene expression. The
CC set of genetic elements produces single stranded DNA with reduced
CC contiguous and intervening nucleotide vector sequences.
XX
SQ Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 24;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accttaaaagcttatacaca 20
|||| ||||||| | ||||
Db 22 ACCTGCAAAGCTTGTGCACA 3

RESULT 9
AAA14544/c
ID AAA14544 standard; DNA; 24 BP.
XX
AC AAA14544;
XX
DT 08-AUG-2000 (first entry)
XX
DE Primer ODN-RT(-) were used to amplify the reverse transcriptase gene.
XX
KW Reverse transcriptase; RNase H; stem-loop structure; genetic element;
KW inverted tandem repeat; vector; inhibitory nucleic acid;
KW antisense sequence; aptamer; gene expression; PCR primer; ss.
XX
OS Moloney murine leukemia virus.
XX
PN WO200022114-A1.
XX
PD 20-APR-2000.
XX
PF 12-OCT-1999; 99WO-US23936.
XX
PR 09-OCT-1998; 98US-0169793.
PR 16-SEP-1999; 99US-0397782.
PR 04-OCT-1999; 99US-0169793.
XX
PA (INGE-) INGENE INC.
XX
PI Conrad CA;
XX
DR WPI; 2000-317974/27.
XX
PT Genetic element for producing and delivering single-stranded DNA,
PT comprises a gene encoding reverse transcriptase and a sequence of
PT interest flanked by an inverted tandem repeat and primer binding site
PT -
XX
PS Example 3; Page 46; 77pp; English.
XX
CC The specification describes methods for producing single-stranded cDNA
CC (sscDNA) in eukaryotic cells. They use a DNA cassette that produces
CC sscDNA in vivo. The cassette contains the Moloney murine leukemia virus
CC reverse transcriptase/RNase H, a bacterial restriction endonuclease
CC gene, and a sequence of interest which produces a RNA template from
CC which the reverse transcriptase synthesises cDNA of a specified
CC sequence. The ssDNA is then modified to remove all flanking vector
CC sequences by taking advantage of the stem-loop structure of the cDNA,
CC which forms as a result of the inclusion of a inverted tandem repeat that
CC allows the sscDNA to fold back on itself, forming a double stranded DNA
CC stem, in the sequence of interest. The double-stranded stem contains one
CC or more functional genetic elements (GE), adapted for incorporation into
CC a vector for delivery to a cell. The vectors are is useful for producing
CC a ssDNA sequence of interest, particularly a cDNA transcript, an
CC inhibitory nucleic acid molecule which is an antisense sequence or
CC aptamer, an mRNA transcript and a heteroduplex molecule. Inhibitory
CC nucleic acid molecules to a target cell are useful for alleviating
CC pathological conditions by regulating gene expression. PCR primers
CC AAA14543-44 were used to amplify the Moloney murine leukemia virus
CC reverse transcriptase coding region.
XX
SQ Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 24;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accttaaaagcttatacaca 20
|||| ||||||| | ||||
Db 22 ACCTGCAAAGCTTGTGCACA 3

RESULT 10
AAA14553/c
ID AAA14553 standard; DNA; 24 BP.
XX
AC AAA14553;
XX
DT 08-AUG-2000 (first entry)
XX
DE Oligonucleotide 3'-RT/Mol-HindIII used to produce expression vectors.
XX
KW Reverse transcriptase; RNase H; stem-loop structure; genetic element;
KW inverted tandem repeat; vector; inhibitory nucleic acid;
KW antisense sequence; aptamer; gene expression; ss.
XX
OS Synthetic.
XX
PN WO200022114-A1.
XX
PD 20-APR-2000.
XX
PF 12-OCT-1999; 99WO-US23936.
XX
PR 09-OCT-1998; 98US-0169793.

PR 16-SEP-1999; 99US-0397782.
PR 04-OCT-1999; 99US-0169793.
XX
PA (INGE-) INGENE INC.
XX
PI Conrad CA;
XX
DR WPI; 2000-317974/27.
XX
PT Genetic element for producing and delivering single-stranded DNA,
PT comprises a gene encoding reverse transcriptase and a sequence of
PT interest flanked by an inverted tandem repeat and primer binding site
PT -
XX
PS Disclosure; Page 47; 77pp; English.
XX
CC The specification describes methods for producing single-stranded cDNA
CC (sscDNA) in eukaryotic cells. They use a DNA cassette that produces
CC sscDNA in vivo. The cassette contains the Moloney murine leukemia virus
CC reverse transcriptase/RNase H, a bacterial restriction endonuclease
CC gene, and a sequence of interest which produces a RNA template from
CC which the reverse transcriptase synthesises cDNA of a specified sequence.
CC The ssDNA is then modified to remove all flanking vector sequences by
CC taking advantage of the stem-loop structure of the cDNA, which forms as
CC a result of the inclusion of a inverted tandem repeat that allows the
CC sscDNA to fold back on itself, forming a double stranded DNA stem, in
CC the sequence of interest. The double-stranded stem contains one or more
CC functional genetic elements (GE), adapted for incorporation into a vector
CC for delivery to a cell. The vectors are is useful for producing a ssDNA
CC sequence of interest, particularly a cDNA transcript, an inhibitory
CC nucleic acid molecule which is an antisense sequence or aptamer, an mRNA
CC transcript and a heteroduplex molecule. Inhibitory nucleic acid molecules
CC to a target cell are useful for alleviating pathological conditions by
CC regulating gene expression. The present oligonucleotide was used to
CC produce vectors for use in the course of the invention.
XX
SQ Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 other;

Query Match 68.0%; Score 13.6; DB 21; Length 24;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accttaaaagcttatacaca 20
|||| ||||||| | ||||
Db 22 ACCTGCAAAGCTTGTGCACA 3

RESULT 11
AAS02282/c
ID AAS02282 standard; DNA; 24 BP.
XX
AC AAS02282;
XX
DT 18-JUL-2001 (first entry)
XX
DE Moloney murine leukaemia virus RNA PCR primer 3'-RT/Mol-HindIII.
XX
KW ODN; oligodeoxynucleotide; inverted tandem repeat; primer binding site;
KW stem-loop; c-myc; viral gene; gene therapy; reverse transcription; ss;
KW endogenous target nucleic acid; gene inactivation; RNA splicing;
KW site-directed mutagenesis; cellular function interruption; PCR primer;
KW nucleic acid duplex binding; nucleic acid triplex binding.
XX
OS Moloney murine leukaemia virus.
XX
PN WO200125419-A1.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000WO-US27381.
XX
PR 04-OCT-1999; 99US-0411568.
PR 28-FEB-2000; 2000US-0514707.
XX
PA (CYTO-) CYTOGENIX INC.
XX
PI Conrad CA, Chen Y;
XX
DR WPI; 2001-266304/27.
XX
PT Alteration of expression of an endogenous nucleic acid for use in gene
PT therapy comprises the expression of a specific antisense sequence -
XX
PS Examples; Page 29; 61pp; English.
XX
CC The sequence represents a PCR primer used to reverse transcribe RNA into
CC single stranded cDNA. This DNA exists in a target cell and is transfected
CC with a cassette comprising a sequence of interest flanked by inverted
CC tandem repeats (ITR) and a primer binding site (PBS) 3' to the tandem
CC repeat. Transcription of the cassette by the target cell produces an RNA
CC template which is reverse transcribed to produce ss-cDNA of a specified
CC sequence. The ss-cDNA folds back on itself as a result of the inverted
CC tandem repeat, to form a stem-loop structure. The loop is comprised of
CC the sequence of interest. The cDNA transcript is bound to an endogenous
CC nucleic acid target to alter expression of the target sequence. This
CC method is useful for altering the expression of gene products e.g. c-myc
CC or a viral gene product. It may be applied to gene therapy, with target
CC genes mutated or introduced for therapeutic purposes, such as gene
CC inactivation using duplex or triplex binding of nucleic acids,
CC site-directed mutagenesis, interruption of cellular function by binding
CC to specific cellular proteins and interfering with RNA splicing
CC functions.
XX
SQ Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 other;

Query Match 68.0%; Score 13.6; DB 22; Length 24;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accttaaaagcttatacaca 20
|||| ||||||| | ||||
Db 22 ACCTGCAAAGCTTGTGCACA 3

RESULT 12
AAS02674/c
ID AAS02674 standard; cDNA; 24 BP.
XX
AC AAS02674;
XX
DT 18-JUL-2001 (first entry)
XX
DE Oligodeoxynucleotide template sequence RT(-).
XX
KW ODN; oligodeoxynucleotide; inverted tandem repeat; primer binding site;
KW stem-loop; c-myc; viral gene; gene therapy; reverse transcription; ss;
KW endogenous target nucleic acid; gene inactivation; RNA splicing;
KW site-directed mutagenesis; cellular function interruption;
KW nucleic acid duplex binding; nucleic acid triplex binding.
XX
OS Synthetic.
XX
PN WO200125419-A1.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000WO-US27381.
XX
PR 04-OCT-1999; 99US-0411568.
PR 28-FEB-2000; 2000US-0514707.
XX
PA (CYTO-) CYTOGENIX INC.
XX
PI Conrad CA, Chen Y;

```
XX
DR   WPI; 2001-266304/27.
XX
PT   Alteration of expression of an endogenous nucleic acid for use in gene
PT   therapy comprises the expression of a specific antisense sequence -
XX
PS   Disclosure; Page 44; 61pp; English.
XX
CC   The sequence represents an oligonucleotide used in the formation of a
CC   plasmid vector producing single stranded cDNA. This DNA exists in a
CC   target cell and is transfected with a cassette comprising a sequence of
CC   interest flanked by inverted tandem repeats (ITR) and a primer binding
CC   site (PBS) 3' to the tandem repeat. Transcription of the cassette by the
CC   target cell produces an RNA template which is reverse transcribed to
CC   produce ss-cDNA of a specified sequence. The ss-cDNA folds back on itself
CC   as a result of the inverted tandem repeat, to form a stem-loop structure.
CC   The loop is comprised of the sequence of interest. The cDNA transcript is
CC   bound to an endogenous nucleic acid target to alter expression of the
CC   target sequence. This method is useful for altering the expression of
CC   gene products e.g. c-myc or a viral gene product. It may be applied to
CC   gene therapy, with target genes mutated or introduced for therapeutic
CC   purposes, such as gene inactivation using duplex or triplex binding of
CC   nucleic acids, site-directed mutagenesis, interruption of cellular
CC   function by binding to specific cellular proteins and interfering with
CC   RNA splicing functions.
XX
SQ   Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 other;


  Query Match             68.0%;  Score 13.6;  DB 22;  Length 24;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 accttaaaagcttatacaca 20
          ||||  ||||||| | ||||
Db     22 ACCTGCAAAGCTTGTGCACA 3


RESULT  13
AAQ32017/c
ID   AAQ32017 standard; DNA; 29 BP.
XX
AC   AAQ32017;
XX
DT   20-APR-1993  (first entry)
XX
DE   86Q3 toxin gene reverse 3' PCR primer.
XX
KW   Toxin protein; ant; polymerase chain reaction; ss.
XX
OS   Synthetic.
XX
PN   WO9220802-A.
XX
PD   26-NOV-1992.
XX
PF   22-MAY-1992;   92WO-US04316.
XX
PR   22-MAY-1991;   91US-0703977.
PR   25-NOV-1991;   91US-0797645.
PR   12-MAY-1992;   92EP-0304228.
XX
PA   (MYCO ) MYCOGEN CORP.
XX
PI   Kennedy MK,  Meier H,  Payne JM,  Randall JB,  Uick HJ;
XX
DR   WPI; 1992-415780/50.
DR   P-PSDB; AAR29033.
XX
PT   Toxin proteins isolated from Bacillus thuringiensis - for controlling
PT   amts. e.g. fire, carpenter, argentine and pharaoh ants
XX
PS   Example; Page 27; 71pp; English.
XX
CC   The oligonucleotide codes for the amino acid sequence ESKLKPNTRY
CC   and can be used as a reverse 3' primer in the amplification of
CC   the 86Q3 toxin gene from Bacillus thurigiensis isolate PS86Q3.
XX
SQ   Sequence 29 BP; 6 A; 3 C; 4 G; 12 T; 4 other;


  Query Match             68.0%;  Score 13.6;  DB 13;  Length 29;
  Best Local Similarity   81.2%;  Pred. No. 1.5e+03;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 ttaaaagcttatacac 19
          ||||||:| :|||||||
Db     20 TTAAAASCGWATACAC 5


RESULT  14
AAQ67666/c
ID   AAQ67666 standard; DNA; 29 BP.
XX
AC   AAQ67666;
XX
DT   19-MAR-1995  (first entry)
XX
DE   PCR primer for delta endotoxin gene from Bacillus thurungiensis.
XX
KW   Corn rootworm; Bacillus thuringiensis; insecticide; amplification; ss.
XX
OS   Synthetic.
XX
PN   WO9416079-A.
XX
PD   21-JUL-1994.
XX
PF   30-DEC-1993;   93WO-US12682.
XX
PR   31-DEC-1992;   92US-0999053.
XX
PA   (MYCO ) MYCOGEN CORP.
XX
PI   Narva KE,  Payne JM;
XX
DR   WPI; 1994-249226/30.
XX
PT   New Bacillus thuringiensis isolates and purified toxins - useful
PT   to control corn rootworm larvae
XX
PS   Example 4; Page 14; 29pp; English.
XX
CC   The sequence is that of a reverse primer for PCR of Bacillus
CC   thuringiensis strain PS80JJ1 cellular DNA to obtain the delta
CC   endotoxin gene. The endotoxin can be used as an
CC   insecticide to control corn rootworms.
CC   See also AAQ67664-7.
XX
SQ   Sequence 29 BP; 6 A; 3 C; 4 G; 12 T; 4 other;


  Query Match             68.0%;  Score 13.6;  DB 15;  Length 29;
  Best Local Similarity   81.2%;  Pred. No. 1.5e+03;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 ttaaaagcttatacac 19
          ||||||:| :|||||||
Db     20 TTAAAASCGWATACAC 5


RESULT  15
AAQ77696/c
ID   AAQ77696 standard; DNA; 29 BP.
XX
AC   AAQ77696;
```

XX
DT 22-JUN-1995 (first entry)
XX
DE B. thuringiensis wireworm-active toxin PS80JJ1 gene primer #2.
XX
KW Bacillus thuringiensis; delta-endotoxin; wireworm; infestation; probe;
KW pHTBlueII; shuttle vector; toxin; crop; crop damage; plant; transgenic;
KW resistance; insect virus; virus; pathogenicity; primer; PCR; amplify; ss.
XX
OS Synthetic.
XX
PN WO9423036-A.
XX
PD 13-OCT-1994.
XX
PF 25-MAR-1994; 94WO-US03308.
XX
PR 26-MAR-1993; 93US-0038759.
XX
PA (MYCO) MYCOGEN CORP.
XX
PI Kim L, Payne J;
XX
DR WPI; 1994-333196/41.
XX
PT Method for controlling wireworm - comprises contacting the
PT wireworms with Bacillus thuringiensis strain.
XX
PS Example 4; Page 18; 37pp; English.
XX
CC Primers (AAQ77695-6) used to amplify a 700-800 bp portion of the gene
CC encoding a novel 130 kD B.thuringiensis delta-endotoxin for the control
CC of wireworm infestations. The sequence was amplified from
CC B.thuringiensis PS80JJ1 total DNA. The resultant fragment was cloned
CC into the plasmid pBluescript S/K and partially sequenced. Sequences
CC unique to PS80JJ1 were identified by comparison with other known
CC delta-endotoxin sequences. The fragment hybridises to a EcoRI fragment
CC of 1.8 kb and a HindIII fragment of 9.5 kb. These bands are thought to
CC contain all or part of the toxin genes. The B.thuringiensis strains
CC PS86A1, PS211B2 or PS80JJ1 or their respective delta-endotoxins can be
CC used to control wireworms which cause damage to crops. Wireworm
CC infestations can also be controlled by introducing the endotoxin genes
CC into the genomes of plants to make the plants resistant to the worms or
CC into insect viruses to enhance their pathogenicity.
XX
SQ Sequence 29 BP; 6 A; 3 C; 4 G; 12 T; 4 other;

Query Match 68.0%; Score 13.6; DB 15; Length 29;
Best Local Similarity 81.2%; Pred. No. 1.5e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy      4 ttaaaagcttatacac 19
          |||||| :|||||||
Db     20 TTAAAASCGWATACAC 5
```

Search completed: March 13, 2002, 10:55:22
Job time: 3869 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 10:55:06 ; Search time 968.42 Seconds
(without alignments)
17.706 Million cell updates/sec

Title: US-09-923-515-29
Perfect score: 20
Sequence: 1 acaccaagggcgaatctcag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15	75.0	15	17	AAT37612	Apo(a) mRNA (nt. p
c	2	15	75.0	15	17	AAT37614	Apo(a) mRNA (nt. p
	3	14.2	71.0	47	21	AAZ69068	Human map-related
c	4	13.8	69.0	22	22	AAH01339	Klebsiella pneumon
c	5	13.8	69.0	28	21	AAA30536	C. tropicalis POX4
c	6	13.8	69.0	57	21	AAA30562	C. tropicalis POX4
	7	13.6	68.0	55	21	AAC17278	Human secreted pro
	8	13.2	66.0	60	19	AAX11589	Human biallelic po
c	9	13	65.0	15	17	AAT37786	Apo(a) mRNA (nt. p
c	10	13	65.0	15	17	AAT37616	Apo(a) mRNA (nt. p
	11	12.8	64.0	32	20	AAZ07798	EIAV RRE 5' elemen
	12	12.8	64.0	32	20	AAX86883	EIAV RRE 5' elemen
	13	12.8	64.0	32	21	AAA12039	EIAV RRE 5'-elemen
	14	12.6	63.0	33	22	AAH57159	Human peroxisome p
	15	12.6	63.0	39	22	AAC86668	PCR primer for inf
	16	12.6	63.0	48	20	AAX90958	Primer-1 used to a
	17	12.6	63.0	59	20	AAX28603	Nucleotide sequenc
	18	12.4	62.0	22	21	AAC61614	Probe specific for
	19	12.2	61.0	18	21	AAZ73087	Human biallelic ma
	20	12.2	61.0	19	16	AAQ98511	Chromosome 14 Alzh
	21	12.2	61.0	29	15	AAQ77888	Neural thread prot
	22	12.2	61.0	31	21	AAA78684	Human genomic DNA
	23	12.2	61.0	41	22	AAF27817	Human HFE gene amp
	24	12.2	61.0	41	22	AAF27835	Human HFE gene amp
c	25	12.2	61.0	46	18	AAT61248	Human antibody hea
c	26	12	60.0	30	19	AAV12074	Human MHC class II
c	27	12	60.0	34	20	AAZ25270	Human FADD PCR pri
	28	12	60.0	37	22	AAS05664	Rat NCAM hybridisa
c	29	12	60.0	40	17	AAT34914	Single stranded DN
c	30	12	60.0	40	17	AAT34912	Single stranded DN
c	31	12	60.0	40	20	AAV73983	Enzymatic DNA 107m
c	32	12	60.0	40	20	AAV73985	Enzymatic DNA 107m
c	33	12	60.0	40	21	AAA92255	DNA enzyme oligonu
c	34	12	60.0	40	21	AAA92257	DNA enzyme oligonu
	35	12	60.0	46	21	AAZ52116	Maize CB1FL19C_u7
	36	12	60.0	46	21	AAZ52192	Primer CB1FL19C_u7
	37	12	60.0	50	20	AAX01599	Probe for human L1
c	38	12	60.0	51	21	AAA76885	Human clone cg3951
	39	12	60.0	55	16	AAT26321	Human gene signatu
c	40	11.8	59.0	17	14	AAQ35932	Human/monkey heavy
c	41	11.8	59.0	17	18	AAT95162	Human or monkey Ig
c	42	11.8	59.0	17	18	AAT91573	Cynomolgus monkey
c	43	11.8	59.0	17	18	AAT62909	IgG1-4 heavy chain
c	44	11.8	59.0	17	19	AAV31421	Cynomolgus immunog
c	45	11.8	59.0	17	19	AAV23800	Primer for Anti-CD

ALIGNMENTS

RESULT 1
AAT37612/c
ID AAT37612 standard; mRNA; 15 BP.
XX
AC AAT37612;
XX
DT 11-NOV-1996 (first entry)
XX
DE Apo(a) mRNA (nt. pos. 10899) hammerhead ribozyme target sequence.
XX
KW Enzymatic RNA molecule; cleavage; apolipoprotein (a); apo(a);
KW hammerhead ribozyme; target sequence; diagnosis; treatment;
KW lipoprotein (a); atherosclerosis; myocardial infarction; stroke;
KW restenosis; heart disease; human; ss.
XX
OS Homo sapiens.
XX
PN WO9609392-A1.
XX
PD 28-MAR-1996.
XX
PF 21-SEP-1995; 95WO-US11995.
XX
PR 23-SEP-1994; 94US-0311760.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI McSwiggen J, Newton RS, Ramharack R, Stinchcomb DT;
XX
DR WPI; 1996-188454/19.
XX
PT Enzymatic RNA mols. which cleave apo(a) mRNA - useful in diagnosis
PT and treatment of conditions related to Lp(a) levels, e.g.
PT atherosclerosis, myocardial infarction, and heart diseases

```
XX
PS   Claim 2; Page 18; 37pp; English.
XX
CC   A claimed enzymatic RNA mol. for the cleavage of apolipoprotein (a)
CC   (apo(a)) mRNA, specifically a hammerhead ribozyme, has binding arms
CC   complementary to the present sequence (nucleotide position 10899).
CC   The ribozyme blocks to some extent apo(a) expression, and can
CC   therefore be used to diagnose or treat conditions related to
CC   lipoprotein (a) levels, e.g. atherosclerosis, myocardial
CC   infarction, stroke, restenosis and heart disease.
CC   PCR was used to generate a substrate for T7 RNA polymerase
CC   transcription from human apo(a) cDNA clones. Labelled transcripts
CC   were synthesised in vitro to form 2 templates. The oligonucleotides
CC   and labelled transcripts were annealed, RNaseH added and the mixts.
CC   incubated. After a designated time the reactions were stopped, and
CC   RNA sepd. on sequencing polyacrylamide gels. The percentage of
CC   substrate cleaved was determined by autoradiographic
CC   quantification, and the most accessible ribozyme target sites
CC   chosen.
XX
SQ   Sequence 15 BP; 2 A; 5 C; 3 G; 5 U; 0 other;


  Query Match             75.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 aagggcgaatctcag 20
          |||||||||||||||
Db     15 AAGGGCGAATCTCAG 1


RESULT   2
AAT37614/c
ID   AAT37614 standard; mRNA; 15 BP.
XX
AC   AAT37614;
XX
DT   11-NOV-1996  (first entry)
XX
DE   Apo(a) mRNA (nt. pos. 10900) hammerhead ribozyme target sequence.
XX
KW   Enzymatic RNA molecule; cleavage; apolipoprotein (a); apo(a);
KW   hammerhead ribozyme; target sequence; diagnosis; treatment;
KW   lipoprotein (a); atherosclerosis; myocardial infarction; stroke;
KW   restenosis; heart disease; human; ss.
XX
OS   Homo sapiens.
XX
PN   WO9609392-A1.
XX
PD   28-MAR-1996.
XX
PF   21-SEP-1995;   95WO-US11995.
XX
PR   23-SEP-1994;   94US-0311760.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   McSwiggen J,  Newton RS,  Ramharack R,  Stinchcomb DT;
XX
DR   WPI; 1996-188454/19.
XX
PT   Enzymatic RNA mols. which cleave apo(a) mRNA - useful in diagnosis
PT   and treatment of conditions related to Lp(a) levels, e.g.
PT   atherosclerosis, myocardial infarction, and heart diseases
XX
PS   Claim 2; Page 18; 37pp; English.
XX
CC   A claimed enzymatic RNA mol. for the cleavage of apolipoprotein (a)
CC   (apo(a)) mRNA, specifically a hammerhead ribozyme, has binding arms
CC   complementary to the present sequence (nucleotide position 10900).
CC   The ribozyme blocks to some extent apo(a) expression, and can
CC   therefore be used to diagnose or treat conditions related to
CC   lipoprotein (a) levels, e.g. atherosclerosis, myocardial
CC   infarction, stroke, restenosis and heart disease.
CC   PCR was used to generate a substrate for T7 RNA polymerase
CC   transcription from human apo(a) cDNA clones. Labelled transcripts
CC   were synthesised in vitro to form 2 templates. The oligonucleotides
CC   and labelled transcripts were annealed, RNaseH added and the mixts.
CC   incubated. After a designated time the reactions were stopped, and
CC   RNA sepd. on sequencing polyacrylamide gels. The percentage of
CC   substrate cleaved was determined by autoradiographic
CC   quantification, and the most accessible ribozyme target sites
CC   chosen.
XX
SQ   Sequence 15 BP; 2 A; 4 C; 4 G; 5 U; 0 other;


  Query Match             75.0%;  Score 15;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 92;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 caagggcgaatctca 19
          |||||||||||||||
Db     15 CAAGGGCGAATCTCA 1


RESULT   3
AAZ69068
ID   AAZ69068 standard; DNA; 47 BP.
XX
AC   AAZ69068;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:3424.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,A)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome  -
XX
PS   Claim 3; Page 961; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
```

CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 11 A; 12 C; 15 G; 9 T; 0 other;

Query Match 71.0%; Score 14.2; DB 21; Length 47;
Best Local Similarity 84.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 caccaagggcgaatctcag 20
|| || || ||||||||||
Db 14 cagcagggacgaatctcag 32

RESULT 4
AAH01339/c
ID AAH01339 standard; DNA; 22 BP.
XX
AC AAH01339;
XX
DT 24-JUL-2001 (first entry)
XX
DE Klebsiella pneumoniae nucleotide sequence SEQ ID NO:1330.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitical;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial;
KW vaccine; primer; ss.
XX
OS Klebsiella pneumoniae.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA01150.
XX
PR 28-SEP-1999; 99CA-2283458.
PR 19-MAY-2000; 2000CA-2307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI; 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
PT archaeal, bacterial, fungal and parasitical species in a test sample -
XX
PS Claim 11; Page 1123; 1580pp; English.
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasitical species, genus, family and group. A nucleic acid (I)
CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexA nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (I) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC which are given in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 4 A; 3 C; 9 G; 6 T; 0 other;

Query Match 69.0%; Score 13.8; DB 22; Length 22;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 acaccaagggcgaatct 17
|||||||| |||||||
Db 17 ACACCAAGTTCGAATCT 1

RESULT 5
AAA30536/c
ID AAA30536 standard; DNA; 28 BP.
XX
AC AAA30536;
XX
DT 21-AUG-2000 (first entry)
XX
DE C. tropicalis POX4A/POX4B QC-RT-PCR primer, SEQ ID NO:51.
XX
KW Cytochrome P450; NADPH reductase; monooxygenase;
KW CYP52A; CPR; POX; omega hydroxylase complex; omega-oxidation;
KW fatty acid; alkane; alpha-omega-dicarboxylic acid production;
KW quantitative competitive reverse transcription-PCR; QC-RT-PCR primer;
KW ss.
XX
OS Candida tropicalis ATCC20366.
XX
PN WO200020566-A2.
XX
PD 13-APR-2000.
XX
PF 10-SEP-1999; 99WO-US20797.
XX
PR 05-OCT-1998; 98US-0103099.
PR 10-MAR-1999; 99US-0123555.
XX
PA (HENK) HENKEL CORP.
XX
PI Wilson CR, Craft DL, Eirich LD, Eshoo M, Madduri KM, Cornett CA;
PI Brenner AA, Tang M, Loper JC, Gleeson M;
XX
DR WPI; 2000-317711/27.
XX
PT Cytochrome P450 nicotine adenine dinucleotide phosphate oxidoreductase
PT and cytochrome P450 monooxygenase nucleic acids and encoded proteins,
PT useful for overproducing dicarboxylic acids -
XX
PS Example 11; Page 44; 200pp; English.
XX
CC The invention relates to 12 novel genomic DNA sequences and proteins
CC which are components of the omega hydroxylase complex of Candida
CC tropicalis ATCC 20366. The DNA sequences (AAA30566-A30577) respectively
CC encode cytochrome P450 NADPH oxidoreductases CPRA and CPRB (AAY90596,

CC AAY90597) and cytochrome P450 monooxygenases CYP52A1A, CYP52A2A,
CC CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B and
CC CYP52D4A (AAY90598-Y90607). Of the cytochrome P450 DNAs isolated, six are
CC unique CYP genes and four are potential alleles. The omega hydroxylase
CC complex is a membrane-bound enzyme complex found in certain yeasts which
CC catalyses the first step in the omega-oxidation of fatty acids or
CC alkanes, this being primary oxidation of the terminal methyl group. Such
CC yeasts, which include members of the genus Candida, excrete
CC alpha-omega-dicarboxylic acids when alkanes or fatty acids are used as
CC the carbon source. The products of the P450 genes CYP52A1, CYP52A2 and
CC CYP52A5 were identified as playing a greater role in the omega-oxidation
CC of long chain fatty acids via a novel quantitative competitive reverse
CC transcription-PCR (QC-RT-PCR). This assay quantifies the amount of target
CC mRNA in a sample and may be used for discriminating members of a gene
CC family, such as the CYP gene family. Organisms containing the target gene
CC are cultured on an organic substrate which causes upregulation of that
CC gene. The total RNA is then extracted and mixed with a known amount of
CC competitor RNA, which is similar to the target mRNA but has fewer
CC nucleotides. RT-PCR reactions are performed using increasing amounts of
CC competitor RNA and the point at which the amount of the corresponding
CC target DNA is equal to the amount of the corresponding competitor DNA is
CC determined. The CPR and CYP nucleic acids may be transformed into a
CC suitable host so that the host overexpresses the corresponding proteins.
CC Such host cells will overproduce dicarboxylic acids. The dicarboxylic
CC acids thus produced find application as thermoplastics, plasticising
CC agents, lubricants, hydraulic fluids, agricultural chemicals,
CC pharmaceuticals, dyes, surfactants, adhesives and fragrances. The CPR and
CC CYR nucleic acids and proteins enable inexpensive large scale production
CC of industrially useful dicarboxylic acids. Sequences AAA30522-A30543
CC represent QC-RT-PCR primers used in an exemplification of the invention
CC to amplify the Candida tropicalis ATCC20366 CPR, CYP and beta-oxidation
CC POX gene target mRNA.
XX
SQ Sequence 28 BP; 6 A; 7 C; 7 G; 8 T; 0 other;

Query Match 69.0%; Score 13.8; DB 21; Length 28;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 accaagggcgaatctca 19
||||| |||| ||||||
Db 26 ACCAATGGCGTATCTCA 10

RESULT 6
AAA30562/c
ID AAA30562 standard; DNA; 57 BP.
XX
AC AAA30562;
XX
DT 21-AUG-2000 (first entry)
XX
DE C. tropicalis POX4A/POX4B competitor RNA QC-RT-PCR primer, SEQ ID NO:77.
XX
KW Cytochrome P450; NADPH reductase; monooxygenase;
KW CYP52A; CPR; POX; omega hydroxylase complex; omega-oxidation;
KW fatty acid; alkane; alpha-omega-dicarboxylic acid production;
KW competitor RNA; quantitative competitive reverse transcription-PCR;
KW QC-RT-PCR primer; ss.
XX
OS Candida tropicalis ATCC20366.
XX
PN WO200020566-A2.
XX
PD 13-APR-2000.
XX
PF 10-SEP-1999; 99WO-US20797.
XX
PR 05-OCT-1998; 98US-0103099.
PR 10-MAR-1999; 99US-0123555.
XX
PA (HENK) HENKEL CORP.
XX
PI Wilson CR, Craft DL, Eirich LD, Eshoo M, Madduri KM, Cornett CA;
PI Brenner AA, Tang M, Loper JC, Gleeson M;
XX
DR WPI; 2000-317711/27.
XX
PT Cytochrome P450 nicotine adenine dinucleotide phosphate oxidoreductase
PT and cytochrome P450 monooxygenase nucleic acids and encoded proteins,
PT useful for overproducing dicarboxylic acids -
XX
PS Example 11; Page 46; 200pp; English.
XX
CC The invention relates to 12 novel genomic DNA sequences and proteins
CC which are components of the omega hydroxylase complex of Candida
CC tropicalis ATCC 20366. The DNA sequences (AAA30566-A30577) respectively
CC encode cytochrome P450 NADPH oxidoreductases CPRA and CPRB (AAY90596,
CC AAY90597) and cytochrome P450 monooxygenases CYP52A1A, CYP52A2A,
CC CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B and
CC CYP52D4A (AAY90598-Y90607). Of the cytochrome P450 DNAs isolated, six are
CC unique CYP genes and four are potential alleles. The omega hydroxylase
CC complex is a membrane-bound enzyme complex found in certain yeasts which
CC catalyses the first step in the omega-oxidation of fatty acids or
CC alkanes, this being primary oxidation of the terminal methyl group. Such
CC yeasts, which include members of the genus Candida, excrete
CC alpha-omega-dicarboxylic acids when alkanes or fatty acids are used as
CC the carbon source. The products of the P450 genes CYP52A1, CYP52A2 and
CC CYP52A5 were identified as playing a greater role in the omega-oxidation
CC of long chain fatty acids via a novel quantitative competitive reverse
CC transcription-PCR (QC-RT-PCR). This assay quantifies the amount of target
CC mRNA in a sample and may be used for discriminating members of a gene
CC family, such as the CYP gene family. Organisms containing the target gene
CC are cultured on an organic substrate which causes upregulation of that
CC gene. The total RNA is then extracted and mixed with a known amount of
CC competitor RNA, which is similar to the target mRNA but has fewer
CC nucleotides. RT-PCR reactions are performed using increasing amounts of
CC competitor RNA and the point at which the amount of the corresponding
CC target DNA is equal to the amount of the corresponding competitor DNA is
CC determined. The CPR and CYP nucleic acids may be transformed into a
CC suitable host so that the host overexpresses the corresponding proteins.
CC Such host cells will overproduce dicarboxylic acids. The dicarboxylic
CC acids thus produced find application as thermoplastics, plasticising
CC agents, lubricants, hydraulic fluids, agricultural chemicals,
CC pharmaceuticals, dyes, surfactants, adhesives and fragrances. The CPR and
CC CYR nucleic acids and proteins enable inexpensive large scale production
CC of industrially useful dicarboxylic acids. Sequences AAA30522-A30543
CC represent QC-RT-PCR primers used in an exemplification of the invention
CC to amplify the Candida tropicalis ATCC20366 CPR, CYP and beta-oxidation
CC POX gene competitor RNA.
XX
SQ Sequence 57 BP; 15 A; 13 C; 15 G; 14 T; 0 other;

Query Match 69.0%; Score 13.8; DB 21; Length 57;
Best Local Similarity 88.2%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 accaagggcgaatctca 19
||||| |||| ||||||
Db 55 ACCAATGGCGTATCTCA 39

RESULT 7
AAC17278
ID AAC17278 standard; cDNA; 55 BP.
XX
AC AAC17278;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 21353.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 21353; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 55 BP; 24 A; 12 C; 10 G; 5 T; 4 other;

Query Match 68.0%; Score 13.6; DB 21; Length 55;
Best Local Similarity 80.0%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 acaccaagggcgaatctcag 20
||| |||| ||||| ||| |
Db 21 acaacaagagcgaaactccg 40

RESULT 8
AAX11589
ID AAX11589 standard; DNA; 60 BP.
XX
AC AAX11589;
XX
DT 30-MAR-1999 (first entry)
XX
DE Human biallelic polymorphic DNA fragment ESTC4.
XX
KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;
KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW treatment; marker; ss.
XX
OS Homo sapiens.
XX
PN WO9820165-A2.
XX
PD 14-MAY-1998.
XX
PF 05-NOV-1997; 97WO-US20313.
XX
PR 06-NOV-1996; 96US-0030455.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Hudson T, Lander ES, Wang D;
XX
DR WPI; 1998-286974/25.
XX
PT New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease
XX
PS Claim 1; Page 174; 310pp; English.
XX
CC AAX10269-X12937 are human DNA fragments which contain biallelic
CC polymorphic markers which have been isolated using the primers
CC represented in AAX09121-X10268. The base occupying the polymorphic site
CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC can be used in methods for determining polymorphic forms in an individual
CC for use in e.g. forensics, paternity testing or for phenotypic typing for
CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC familial hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases.
XX
SQ Sequence 60 BP; 24 A; 14 C; 8 G; 13 T; 1 other;

Query Match 66.0%; Score 13.2; DB 19; Length 60;
Best Local Similarity 78.9%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 acaccaagggcgaatctca 19
||| || || | |||||||
Db 13 acaacatggacnaatctca 31

RESULT 9
AAT37786/c
ID AAT37786 standard; mRNA; 15 BP.
XX
AC AAT37786;
XX
DT 18-NOV-1996 (first entry)
XX
DE Apo(a) mRNA (nt. pos. 11098) hammerhead ribozyme target sequence.
XX
KW Enzymatic RNA molecule; cleavage; apolipoprotein (a); apo(a);
KW hammerhead ribozyme; target sequence; diagnosis; treatment;
KW lipoprotein (a); atherosclerosis; myocardial infarction; stroke;
KW restenosis; heart disease; monkey; ss.
XX
OS Cebus apella.
XX
PN WO9609392-A1.
XX
PD 28-MAR-1996.
XX
PF 21-SEP-1995; 95WO-US11995.
XX
PR 23-SEP-1994; 94US-0311760.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX

PI McSwiggen J, Newton RS, Ramharack R, Stinchcomb DT;
XX
DR WPI; 1996-188454/19.
XX
PT Enzymatic RNA mols. which cleave apo(a) mRNA - useful in diagnosis
PT and treatment of conditions related to Lp(a) levels, e.g.
PT atherosclerosis, myocardial infarction, and heart diseases
XX
PS Claim 3; Page 21; 37pp; English.
XX
CC A claimed enzymatic RNA mol. for the cleavage of apolipoprotein (a)
CC (apo(a)) mRNA, specifically a hammerhead ribozyme, has binding arms
CC complementary to the present sequence (nucleotide position 11098).
CC The ribozyme blocks to some extent apo(a) expression, and can
CC therefore be used to diagnose or treat conditions related to
CC lipoprotein (a) levels, e.g. atherosclerosis, myocardial
CC infarction, stroke, restenosis and heart disease.
CC PCR was used to generate a substrate for T7 RNA polymerase
CC transcription from monkey apo(a) cDNA clones. Labelled transcripts
CC were synthesised in vitro to form 2 templates. The oligonucleotides
CC and labelled transcripts were annealed, RNaseH added and the mixts.
CC incubated. After a designated time the reactions were stopped, and
CC RNA sepd. on sequencing polyacrylamide gels. The percentage of
CC substrate cleaved was determined by autoradiographic
CC quantification, and the most accessible ribozyme target sites
CC chosen.
XX
SQ Sequence 15 BP; 1 A; 4 C; 4 G; 6 U; 0 other;

Query Match 65.0%; Score 13; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acaccaagggcga 13
||||||||||||
Db 13 ACACCAAGGGCGA 1

RESULT 10
AAT37616/c
ID AAT37616 standard; mRNA; 15 BP.
XX
AC AAT37616;
XX
DT 11-NOV-1996 (first entry)
XX
DE Apo(a) mRNA (nt. pos. 10906) hammerhead ribozyme target sequence.
XX
KW Enzymatic RNA molecule; cleavage; apolipoprotein (a); apo(a);
KW hammerhead ribozyme; target sequence; diagnosis; treatment;
KW lipoprotein (a); atherosclerosis; myocardial infarction; stroke;
KW restenosis; heart disease; human; ss.
XX
OS Homo sapiens.
XX
PN WO9609392-A1.
XX
PD 28-MAR-1996.
XX
PF 21-SEP-1995; 95WO-US11995.
XX
PR 23-SEP-1994; 94US-0311760.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI McSwiggen J, Newton RS, Ramharack R, Stinchcomb DT;
XX
DR WPI; 1996-188454/19.
XX
PT Enzymatic RNA mols. which cleave apo(a) mRNA - useful in diagnosis
PT and treatment of conditions related to Lp(a) levels, e.g.
PT atherosclerosis, myocardial infarction, and heart diseases
XX
PS Claim 2; Page 18; 37pp; English.
XX
CC A claimed enzymatic RNA mol. for the cleavage of apolipoprotein (a)
CC (apo(a)) mRNA, specifically a hammerhead ribozyme, has binding arms
CC complementary to the present sequence (nucleotide position 10906).
CC The ribozyme blocks to some extent apo(a) expression, and can
CC therefore be used to diagnose or treat conditions related to
CC lipoprotein (a) levels, e.g. atherosclerosis, myocardial
CC infarction, stroke, restenosis and heart disease.
CC PCR was used to generate a substrate for T7 RNA polymerase
CC transcription from human apo(a) cDNA clones. Labelled transcripts
CC were synthesised in vitro to form 2 templates. The oligonucleotides
CC and labelled transcripts were annealed, RNaseH added and the mixts.
CC incubated. After a designated time the reactions were stopped, and
CC RNA sepd. on sequencing polyacrylamide gels. The percentage of
CC substrate cleaved was determined by autoradiographic
CC quantification, and the most accessible ribozyme target sites
CC chosen.
XX
SQ Sequence 15 BP; 1 A; 4 C; 4 G; 6 U; 0 other;

Query Match 65.0%; Score 13; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acaccaagggcga 13
||||||||||||
Db 13 ACACCAAGGGCGA 1

RESULT 11
AAZ07798
ID AAZ07798 standard; DNA; 32 BP.
XX
AC AAZ07798;
XX
DT 23-NOV-1999 (first entry)
XX
DE EIAV RRE 5' element amplifying primer ERRE1.
XX
KW Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
KW prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor;
KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria; ss;
KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; EIAV; PCR primer.
XX
OS Synthetic.
OS Equine infectious anemia virus.
XX
PN WO9945126-A2.
XX
PD 10-SEP-1999.
XX
PF 05-MAR-1999; 99WO-GB00672.
XX
PR 06-MAR-1998; 98GB-0004841.
PR 19-AUG-1998; 98GB-0018103.
PR 29-JAN-1999; 99GB-0002081.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
PI Mitrophanous K;
XX
DR WPI; 1999-540852/45.
XX
PT New prodrug activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors or inflammation -
XX
PS Example 14B; Page 101; 149pp; English.
XX
CC The invention provides a new prodrug activating agent that comprises:

CC (i) a localization domain (LD; other than a tumor-selective antibody) and
CC a prodrug activating domain (PAD); (ii) at least one nucleic acid
CC encoding a cytochrome P450 and under control of at least one constitutive
CC or inducible expression control sequence or (iii) a modified
CC hematopoietic stem cell (MHSC) containing at least one nucleic acid
CC encoding a PAD and under control of elements as in (ii). The prodrug
CC activating agent or vectors that express them, are specifically used to
CC treat tumors, inflammation, atherosclerosis and muscular dystrophy, but
CC may also be used to treat many other conditions, e.g. cerebral malaria,
CC rheumatoid arthritis, or conditions associated with hypoxia, hypoglycemia
CC or ischemia, or to deliver antibiotics, antiviral agents, analgesics,
CC anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
CC locations or by delivering it to neighboring cells (bystander effect),
CC and allow a reduction in dose of prodrug, and thus of systemic side-
CC effects. Nucleic acids encoding the agent may be expressed selectively
CC in hypoxic cells. Sequences AAZ07798-99 represent PCR primers for
CC amplifying EIAV RRE 5' element. This is used for constructing EIAV
CC vectors expressing P450.
XX
SQ Sequence 32 BP; 8 A; 9 C; 8 G; 7 T; 0 other;

Query Match 64.0%; Score 12.8; DB 20; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ccaagggcgaatctca 19
|| |||| ||||||||
Db 15 cccagggggaatctca 30

RESULT 12
AAX86883
ID AAX86883 standard; DNA; 32 BP.
XX
AC AAX86883;
XX
DT 20-SEP-1999 (first entry)
XX
DE EIAV RRE 5' element amplifying primer ERRE1.
XX
KW Retroviral vector; non-primate; lentivirus; gag gene; tat gene; LTR;
KW long terminal repeat; gene therapy; Equine infectious anemia virus;
KW EIAV; HIV infection; PCR primer; ss.
XX
OS Synthetic.
OS Equine infectious anemia virus.
XX
PN WO9932646-A1.
XX
PD 01-JUL-1999.
XX
PF 22-DEC-1998; 98WO-GB03876.
XX
PR 22-MAY-1998; 98GB-0011037.
PR 22-DEC-1997; 97GB-0027135.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Carroll MW, Kim N, Kingsman AJ, Mitrophanous K;
PI Rohll J;
XX
DR WPI; 1999-418936/35.
XX
PT Retroviral vectors derived from a non-primate lentivirus genome
XX
PS Example 3; Page 37; 124pp; English.
XX
CC The invention provides retroviral vectors derived from a non-primate
CC lentivirus genome. These vectors comprise a deleted gag gene. The
CC deletion in gag removes one or more nucleotides downstream of nucleotide
CC 350 of the gag coding sequence. One or more accessory genes are absent
CC from the non-primate lentivirus genome or lack the tat gene but includes
CC the leader sequences between the end of the 5' long terminal repeat (LTR)
CC and the ATG of gag. The vectors, particles or cells transfected with
CC either of these, are useful for the delivery of nucleotides of interest
CC to a target site (i.e. gene therapy). The retroviral vector can be used
CC as a delivery system. Alternatively, a non-retroviral expression vector,
CC adenovirus or plasmid can be used as a delivery system for the retroviral
CC vector. The retroviral vectors are capable of transferring genetic
CC material to non-dividing or slowly dividing cells. Deletion of larger
CC regions of the gag gene in Equine infectious anemia virus (EIAV) vectors
CC is advantageous and leads to higher titers of viral vector being
CC produced. Deletion of accessory genes permits vectors to be produced
CC without the genes normally associated with disease in lentiviral (e.g.
CC HIV) infections. The deletion of these genes also permits the vector to
CC package more heterologous DNA.
XX
SQ Sequence 32 BP; 8 A; 9 C; 8 G; 7 T; 0 other;

Query Match 64.0%; Score 12.8; DB 20; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ccaagggcgaatctca 19
|| |||| ||||||||
Db 15 cccagggggaatctca 30

RESULT 13
AAA12039
ID AAA12039 standard; DNA; 32 BP.
XX
AC AAA12039;
XX
DT 14-AUG-2000 (first entry)
XX
DE EIAV RRE 5'-element PCR primer ERRE1.
XX
KW HRE; hypoxia response element; hypoxia-inducible factor; HIF; vasotropic;
KW cardiant; cytostatic; antiarthritic; gene therapy; ischaemia; arthritis;
KW cardiovascular disease; peripheral arterial disease; cancer; human;
KW PCR primer; ss.
XX
OS Equine infectious anemia virus.
XX
PN WO200017371-A1.
XX
PD 30-MAR-2000.
XX
PF 22-SEP-1999; 99WO-GB03181.
XX
PR 23-SEP-1998; 98WO-GB02885.
PR 28-JAN-1999; 99GB-0001906.
PR 16-FEB-1999; 99GB-0003538.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Binley KM, Naylor S;
XX
DR WPI; 2000-283595/24.
XX
PT Novel polynucleotide constructs comprising at least two repeats of a
PT hypoxia response element useful for driving expression of nucleic acids
PT of interest in a cell under hypoxic conditions -
XX
PS Example 9; Page 87; 155pp; English.
XX
CC This invention describes novel polynucleotide comprising at least 2
CC repeats of a hypoxia response element (HRE), where the hypoxia-inducible
CC factor (HIF) consensus binding sites within each of the 2 repeats are
CC separated by a spacer of at least 20 contiguous nucleotides. The products
CC of the invention have vasotropic, cardiant, cytostatic and antiarthritic
CC activity and can be used for gene therapy. The polynucleotides are useful

CC for delivering nucleic acids of interest to mammalian cells. Lentiviral
CC vectors are responsive to hypoxic agents and to agents that mimic
CC hypoxia. This regulation can be harnessed in vitro to enhance the
CC production of the vector and can be used in vivo to regulate gene
CC expression in response to a physiological signal. The vectors have
CC utility in disease, where ischaemia, including hypoxia, is a feature,
CC e.g. cardiovascular disease, peripheral arterial disease, cancer and
CC arthritis. The novel regulatory construct is capable of driving very high
CC levels of transcription under conditions of hypoxia whilst providing only
CC low basal levels of transcription under normal oxygen conditions. The
CC polynucleotide construct targets cells within a tumor mass that are under
CC conditions of hypoxia without affecting normal surrounding tissue. This
CC sequence represents a PCR primer used in the amplification of the equine
CC infectious anemia virus RRE 5'-element region which is used in the
CC method of the invention.
XX
SQ Sequence 32 BP; 8 A; 9 C; 8 G; 7 T; 0 other;

Query Match 64.0%; Score 12.8; DB 21; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ccaagggcgaatctca 19
|| |||| ||||||||
Db 15 cccaggggggaatctca 30

RESULT 14
AAH57159
ID AAH57159 standard; DNA; 33 BP.
XX
AC AAH57159;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human peroxisome proliferator-activated receptor protein PCR primer 3.
XX
KW Ligand dependent transcriptional factor; oestrogen receptor; ER;
KW glucocorticoid receptor protein; GR; mineralocorticoid receptor protein;
KW MR; peroxisome proliferator-activated receptor protein; PPAR;
KW progesterone receptor protein; PR; pregnane X receptor protein; PXR;
KW thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR;
KW transactivation; ERalpha; breast cancer; PCR primer; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200142307-A1.
XX
PD 14-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-JP08553.
XX
PR 07-DEC-1999; 99JP-0348022.
PR 27-DEC-1999; 99JP-0370667.
PR 07-JUL-2000; 2000JP-0207011.
PR 21-JUL-2000; 2000JP-0220508.
PR 02-AUG-2000; 2000JP-0234053.
PR 03-AUG-2000; 2000JP-0235460.
PR 03-AUG-2000; 2000JP-0235461.
PR 03-AUG-2000; 2000JP-0235463.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Saito K, Ohe N, Satoh H;
XX
DR WPI; 2001-367866/38.
XX
PT Ligand dependent transcriptional factors, nucleic acids encoding them
PT and cells comprising them and a specified reporter gene, useful for
PT screening agents for the treatment of breast cancer -
XX
PS Example 29; Page 268; 276pp; English.
XX
CC The present invention relates to ligand dependent transcriptional factors
CC including oestrogen receptor (ER) alpha and beta protein, glucocorticoid
CC receptor protein (GR), mineralocorticoid receptor protein (MR),
CC peroxisome proliferator-activated receptor protein (PPAR), progesterone
CC receptor protein (PR), pregnane X receptor protein (PXR), thyroid hormone
CC receptor protein (TR) and vitamin D receptor protein (VDR), the nucleic
CC acids encoding them and cells comprising them and a specified reporter
CC gene for the ligand dependent transcriptional factor. These proteins are
CC useful in the modulation of ligand dependent transcriptional factor
CC activity. The cells, mutant ERalpha and the polynucleotide encoding it
CC may be used in assays for qualitatively analysing an activity for
CC transactivation of a reporter gene by a test ERalpha, for screening
CC mutant ligand dependent transcriptional factors, for evaluating an
CC activity for transactivation of a reporter gene by a test ERalpha and/or
CC for screening a compound useful for treating a disorder of a mutant
CC ERalpha, especially breast cancer.
XX
SQ Sequence 33 BP; 8 A; 9 C; 8 G; 8 T; 0 other;

Query Match 63.0%; Score 12.6; DB 22; Length 33;
Best Local Similarity 78.9%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 caccaagggcgaatctcag 20
||||| ||| ||| ||| |
Db 2 caccatgggtgaaactctg 20

RESULT 15
AAC86668
ID AAC86668 standard; DNA; 39 BP.
XX
AC AAC86668;
XX
DT 02-APR-2001 (first entry)
XX
DE PCR primer for infectious Hepatitis C virus strain HC-J6CH.
XX
KW HCV; HCV strain HC-J6CH; HCV genotype 2a; antiviral; vaccine;
KW PCR primer; ss.
XX
OS Hepatitis C virus.
XX
PN WO200075338-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US15446.
XX
PR 04-JUN-1999; 99US-0137693.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Yanagi M, Bukh J, Emerson SU, Purcell RH;
XX
DR WPI; 2001-061728/07.
XX
PT Nucleic acid molecule encoding human hepatitis C virus of genotype 2a
PT for developing vaccines, for diagnosis of hepatitis C virus and in
PT screening assays for identification of antiviral agents -
XX
PS Disclosure; Page 30; 167pp; English.
XX
CC The present sequence represents a PCR primer used for amplification
CC and cloning of nucleic acid sequences from infectious Hepatitis C virus
CC (HCV) strain HC-J6CH genotype 2a. The HCV polynucleotide sequence is
CC capable of expressing the virus when transfected into cells. The HCV
CC protein is useful for assaying candidate antiviral agents for activity
CC against HCV. Antibodies specific for HCV polypeptide are useful in
CC prevention and treatment of diseases caused by HCV in animals, in
CC particular humans. The HCV polypeptides serve as immunogens in the

CC development of vaccines for preventing HCV in mammals or as antigens
CC in diagnostic assays for detecting the presence of HCV in biological
CC samples. The HCV polynucleotide is also useful for identifying cell
CC lines capable of supporting the replication of HCV in vitro and to
CC produce attenuated viral strains via passage in vitro or in vivo.
XX
SQ Sequence 39 BP; 8 A; 11 C; 12 G; 8 T; 0 other;

Query Match 63.0%; Score 12.6; DB 22; Length 39;
Best Local Similarity 78.9%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1 acaccaagggcgaatctca 19
           || || ||||||  |||||
Db      11 acccctagggcggctctca 29
```

Search completed: March 13, 2002, 10:55:08
Job time: 3855 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 09:50:44 ; Search time 1263.07 Seconds
(without alignments)
13.575 Million cell updates/sec

Title: US-09-923-515-26
Perfect score: 20
Sequence: 1 ccatctgacattgggatcca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn/NA1988.DAT:*
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11: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13.8	69.0	28	18	AAV05105	Primer sequence co
2	13.8	69.0	31	22	AAH46572	Arabidopsis thalia
c 3	13.8	69.0	36	19	AAV59476	S. cerevisiae 2-DO
c 4	13.8	69.0	36	22	AAH21134	Tagetes patula DOG
c 5	13.6	68.0	20	18	AAT94350	Human DPC4 sequenc
c 6	13.6	68.0	26	13	AAQ24142	PCR primer p-a01.
c 7	13.6	68.0	26	14	AAQ41891	Factor Xa inhibiti
8	13.4	67.0	25	17	AAT36048	Murine InK4D-p19 g
c 9	13.4	67.0	30	18	AAT65534	Oligonucleotide 12
c 10	13.4	67.0	30	18	AAT63004	c-mpl receptor ago
c 11	13.4	67.0	30	19	AAV55446	Primer 123-5' for
12	13.4	67.0	43	21	AAA10268	PSMA monoclonal an
c 13	13.2	66.0	36	22	AAF90190	PCR primer for DNA
c 14	13	65.0	15	17	AAT37559	Apo(a) mRNA (nt. p
c 15	12.8	64.0	18	21	AAZ74940	Human biallelic ma
c 16	12.8	64.0	41	16	AAQ99692	Bovine viral diarr
c 17	12.8	64.0	42	16	AAT05155	Prepro-hK2 kallikr
c 18	12.8	64.0	42	17	AAT58203	Prostate-specific
c 19	12.8	64.0	42	18	AAT72143	Human Her-3 solubl
c 20	12.8	64.0	42	19	AAV70337	Prostate-specific
c 21	12.8	64.0	42	19	AAV32942	Human Kallikrein 2
c 22	12.8	64.0	42	19	AAV06607	Prostate-specific
c 23	12.8	64.0	46	16	AAT01156	Influenza virus he
c 24	12.6	63.0	25	16	AAQ96260	Rat smooth muscle
c 25	12.6	63.0	25	20	AAX05453	CEA6 scFV antibody
c 26	12.6	63.0	27	18	AAT74669	Pig myogenin gene
c 27	12.6	63.0	29	16	AAQ89542	Cold tolerance Wcs
c 28	12.6	63.0	29	18	AAT45946	Human hypoxia indu
c 29	12.6	63.0	29	19	AAV20394	Primer for CKR-5 m
30	12.6	63.0	33	20	AAZ28879	Oligonucleotide #2
c 31	12.6	63.0	38	22	AAH02378	Human Factor V PCR
c 32	12.6	63.0	42	17	AAT13101	CFTR gene intron 1
c 33	12.6	63.0	42	19	AAV39870	Streptococcus pneu
c 34	12.6	63.0	45	18	AAT58884	Monospecific tetra
35	12.4	62.0	18	17	AAT16410	Primer #1 for sWSS
36	12.4	62.0	18	21	AAC62605	Human OB gene sequ
37	12.4	62.0	18	21	AAC62685	Human OB gene sequ
38	12.4	62.0	18	21	AAA12327	Human OB DNA PCR p
39	12.4	62.0	20	22	AAH21419	C. lanceolata KASI
c 40	12.4	62.0	20	22	AAF63778	PCR primer specifi
c 41	12.4	62.0	21	20	AAZ23437	Human p75NTR depen
42	12.4	62.0	29	19	AAV40510	Human secreted pro
c 43	12.4	62.0	29	19	AAV11731	Human G-protein co
c 44	12.4	62.0	29	19	AAT89988	Primer HTLCA-F for
c 45	12.4	62.0	29	19	AAT94189	Primer HTLCA-F for

ALIGNMENTS

RESULT 1
AAV05105/c
ID AAV05105 standard; DNA; 28 BP.
XX
AC AAV05105;
XX
DT 13-MAY-1998 (first entry)
XX
DE Primer sequence corresponding to the M gene of CDV strain OP.
XX
KW CDV; strain A75/17; Morbillivirus; nucleocapsid gene; N gene;
KW fusion protein gene; F gene; haemagglutinin gene; H gene; antigen;
KW CDV-specific; immune response; prophylactic vaccine; dog; human;
KW neutralising antibody; protective response; Paget's disease;
KW OP-CDV; matrix gene; M gene; ss.
XX
OS Synthetic.
OS Canine distemper virus.
XX
PN WO9741236-A1.
XX
PD 06-NOV-1997.
XX
PF 28-APR-1997; 97WO-IB00444.
XX
PR 29-APR-1996; 96EP-0810273.
XX
PA (WITT/) WITTEK R.
PA (ZURB/) ZURBRIGGEN A.
XX
PI Wittek R, Zurbriggen A;
XX
DR WPI; 1997-549738/50.
XX

PT Nucleic acid construct expressing immunogenic canine distemper virus
PT protein - useful in vaccines, inducing both humoral and cellular
PT immune responses
XX
PS Example 1; Page 29; 58pp; English.
XX
CC Primers AAV05103-12 were used for the first strand cDNA synthesis of the
CC genome of canine distemper virus (CDV) strain A75/17 (wild type). RNA
CC was extracted from primary dog cell cultures infected with CDV. The RNA
CC was reverse transcribed using the above primers, which correspond to
CC regions which are highly conserved in Morbilliviruses. Double stranded
CC cDNA was cloned into pCRII, and the genes encoding the nucleocapsid
CC (N gene), the fusion protein (F gene) and the haemagglutinin gene
CC (H gene) were isolated. These genes were amplified, and inserted into
CC vectors to produce new nucleic acid constructs that can express, in vivo
CC in animal tissue, at least one antigenic product of CDV, inducing a
CC CDV-specific immune response. These constructs are useful as
CC prophylactic vaccines to induce neutralising antibodies, cytotoxic
CC lymphocytes and protective responses against CDV in mammals, preferably
CC carnivores and specifically dogs or humans (CDV has been implicated in
CC Paget's disease). Nucleic acid vaccines induce both cellular and humoral
CC immunity, do not involve live virus, and cannot revert to virulence.
XX
SQ Sequence 28 BP; 10 A; 6 C; 7 G; 5 T; 0 other;

Query Match 69.0%; Score 13.8; DB 18; Length 28;
Best Local Similarity 88.2%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tctgacattgggatcca 20
|||||| | ||||||||
Db 20 TCTGACTTGGGGATCCA 4

RESULT 2
AAH46572
ID AAH46572 standard; DNA; 31 BP.
XX
AC AAH46572;
XX
DT 13-SEP-2001 (first entry)
XX
DE Arabidopsis thaliana chloroplastferrochelatase gene PCR primer #1.
XX
KW Arabidopsis; herbicide resistance; protoporphylinogen IX oxidase;
KW PPO IX; transgenic plant; chloroplastferrochelatase; PCR primer; ss.
XX
OS Arabidopsis thaliana.
XX
PN JP2001120092-A.
XX
PD 08-MAY-2001.
XX
PF 29-OCT-1999; 99JP-0310245.
XX
PR 29-OCT-1999; 99JP-0310245.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
DR WPI; 2001-459933/50.
XX
PT Protoporphylinogen IX oxidase-inhibiting herbicide-resistant
PT agricultural plants -
XX
PS Example 2; Page 40; 43pp; Japanese.
XX
CC The invention relates to a herbicide-resistant protoporphylinogen IX
CC oxidase (PPO IX)-active plant. A gene has been introduced into the
CC plant and the gene is expressed to generate a herbicide-resistant plant.
CC The present sequence is a PCR primer used to amplify the Arabidopsis
CC chloroplastferrochelatase gene in an example to illustrate the
CC invention.
XX
SQ Sequence 31 BP; 7 A; 6 C; 9 G; 9 T; 0 other;

Query Match 69.0%; Score 13.8; DB 22; Length 31;
Best Local Similarity 88.2%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tctgacattgggatcca 20
||||| ||| |||||||
Db 8 tctgaaatttggatcca 24

RESULT 3
AAV59476/c
ID AAV59476 standard; cDNA; 36 BP.
XX
AC AAV59476;
XX
DT 15-JAN-1999 (first entry)
XX
DE S. cerevisiae 2-DOG-6-P phosphatase PCR primer DOG-R1-1.
XX
KW 2-Deoxyglucose-6-phosphate phosphatase; 2-DOG-6-P phosphatase; yeast;
KW promoter; terminator; vector; selectable marker; foreign gene; plant;
KW Agrobacterium transformation; particle bombardment; PCR primer; ss.
XX
OS Synthetic.
OS Saccharomyces cerevisiae.
XX
PN EP870836-A1.
XX
PD 14-OCT-1998.
XX
PF 09-APR-1997; 97EP-0105855.
XX
PR 09-APR-1997; 97EP-0105855.
XX
PA (IPKG-) IPK GATERSLEBEN.
XX
PI Ebneth M, Sonnewald U;
XX
DR WPI; 1998-523161/45.
XX
PT Plant transformation vector containing selectable marker - which is
PT yeast 2-deoxy-glucose-6-phosphate phosphatase gene for selection in
PT 2-deoxy-glucose media
XX
PS Example 2; Page 10; 27pp; German.
XX
CC AAV59476 and AAV59477 are PCR primers used in the amplification of a
CC yeast 2-deoxyglucose-6-phosphate phosphatase, (2-DOG-6-P phosphatase)
CC which can be linked to a plant promoter and a plant terminator and/or
CC polyadenylation signal to construct novel vectors. Such vectors
CC containing the 2-DOG-6-P phosphatase DNA as a selectable marker can be
CC used to introduce foreign genes into plant cells, especially by
CC Agrobacterium transformation or particle bombardment, transformants
CC being selected in a medium containing 2-deoxyglucose.
XX
SQ Sequence 36 BP; 9 A; 8 C; 8 G; 11 T; 0 other;

Query Match 69.0%; Score 13.8; DB 19; Length 36;
Best Local Similarity 88.2%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tctgacattgggatcca 20
|||| ||| |||||||
Db 18 TCTGCCATGGGGATCCA 2

RESULT 4
AAH21134/c

ID AAH21134 standard; DNA; 36 BP.
XX
AC AAH21134;
XX
DT 06-SEP-2001 (first entry)
XX
DE Tagetes patula DOGR1 PCR primer DOGR1-1.
XX
KW DOGR1; transgenic plant; nematocide; fungicide; insecticide; food;
KW thiophene; flavonoid; carotenoid antioxidant; coloring agent;
KW cosmetic; antifungal agent; Vitamin A; anticancer agent; PCR primer; ss.
XX
OS Tagetes patula.
XX
PN WO200146445-A2.
XX
PD 28-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-EP12643.
XX
PR 21-DEC-1999; 99DE-1062133.
XX
PA (SUNG-) SUNGENE GMBH & CO KGAA.
XX
PI Kunze I, Herbers K, Heim U;
XX
DR WPI; 2001-408651/43.
XX
PT Method for stably transforming Tagetes, useful for producing strains
PT with increased production of carotenoids and other biologically active
PT metabolites -
XX
PS Example 5; Page 11; 19pp; German.
XX
CC This invention describes a novel method for preparing stably transformed,
CC fertile plants of the genus Tagetes by (i) growing plants and recovering
CC suitable explants; (ii) transfer of DNA to the plant cells; (iii)
CC selection of transformed cells and (iv) regeneration to (A). The method
CC is used to produce strains of Tagetes with improved production of (i)
CC nematocides, fungicides and insecticides (e.g. thiophene derivatives) or
CC (ii) flavonoids and carotenoids (variously useful as antioxidants,
CC coloring agents for cosmetics and foods, antifungal agents, Vitamin A and
CC potential anticancer agents). Genetic modification of Tagetes avoids the
CC limitation of low genetic variability within the genus which makes it
CC difficult to develop new strains by classical breeding methods. This
CC sequence represents a PCR primer used in the amplification of the Tagetes
CC patula DOGR1 gene described in the method of the invention.
XX
SQ Sequence 36 BP; 9 A; 8 C; 8 G; 11 T; 0 other;

Query Match 69.0%; Score 13.8; DB 22; Length 36;
Best Local Similarity 88.2%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 tctgacattgggatcca 20
|||| ||| ||||||||
Db 18 TCTGCCATGGGGATCCA 2

RESULT 5
AAT94350/c
ID AAT94350 standard; DNA; 20 BP.
XX
AC AAT94350;
XX
DT 04-MAR-1998 (first entry)
XX
DE Human DPC4 sequence tagged site antisense primer D18S474.
XX
KW DPC4; pancreatic cancer; deleted; locus 4; diagnosis; human;
KW tumour suppressor gene; proliferative disease; PCR primer;
KW sequence tagged site; STS; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9726271-A1.
XX
PD 24-JUL-1997.
XX
PF 17-JAN-1997; 97WO-US00827.
XX
PR 19-JAN-1996; 96US-0588821.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Hahn SA, Kern SE;
XX
DR WPI; 1997-385290/35.
XX
PT Deleted in Pancreatic Cancer locus 4 polypeptide - and related
PT nucleic acids, used in diagnosis and treatment of proliferative
PT diseases, e.g. cancer of pancreas or other organs
XX
PS Example 2; Page 56; 104pp; English.
XX
CC The present sequence represents a sequence tagged site (STS) primer used
CC in the isolation of cosmids from the DPC4 (deleted in pancreatic cancer,
CC locus 4) region, and gene identification. DPC4 is a tumour suppressor
CC gene. Detection of truncated DPC4 protein, or of homozygous deletions or
CC intragenic mutations in nucleic acid encoding it, is used to diagnose
CC (in vivo or in vitro) proliferative diseases, especially pancreatic
CC carcinoma, bile duct, bladder or colorectal cancer, Crohn's disease,
CC colitis-associated neoplasia or chronic ulcerative colitis. These
CC conditions, where associated with a homozygous deletion, can be treated
CC by administering an agent that: (a) modulates DPC4 expression,
CC specifically a sense DPC4 sequence (particularly in the form of a
CC vector, i.e. by gene therapy), but also an antisense sequence where DPC4
CC protein is over expressed or (b) mimics the activity of DPC4. DPC4
CC nucleic acid is also used as hybridisation probes for detecting
CC presence/absence of human chromosome 18q21.1 fragments. When a
CC homozygous deletion is detected in this region, an agent can be
CC administered that accumulates within, or kills, only cells which
CC contain such a deletion. This agent exploits the absence of an enzyme
CC (or other protein) encoded by a neighbouring gene and lost by the
CC deletion, i.e. it has a highly selective action.
XX
SQ Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 other;

Query Match 68.0%; Score 13.6; DB 18; Length 20;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ccatctgacattgggatcca 20
|| |||||||||| | |||
Db 20 CCTTCTGACATTGAAAGCCA 1

RESULT 6
AAQ24142/c
ID AAQ24142 standard; DNA; 26 BP.
XX
AC AAQ24142;
XX
DT 15-NOV-1992 (first entry)
XX
DE PCR primer p-a01.
XX
KW Polymerase chain reaction; p-s01; UTI; TN70; EaeI; BamHI; ss.
XX
OS Synthetic.
XX
PN EP486001-A.
XX

PD 20-MAY-1992.
XX
PF 13-NOV-1991; 91EP-0119378.
XX
PR 13-NOV-1990; 90JP-0306745.
XX
PA (MOCH) MOCHIDA PHARM CO LTD.
XX
PI Kanamori T, Morishita H, Nobuhara M;
XX
DR WPI; 1992-168622/21.
XX
PT New polypeptides comprise amino acid sequence of urinary trypsin
PT inhibitor - are protease inhibitors for treating e.g. ischaemic
PT heart disease, thrombosis, arthritis, allergy, shock, etc.
XX
PS Disclosure; Fig 4b; 106pp; English.
XX
CC The sequences given in AAQ24141-2 are primers used to amplify the DNA
CC encoding a novel polypeptide which comprises the amino acid sequence
CC that constitutes a portion of urinary trypsin inhibitor (UTI). The
CC DNA encoding the polypeptide of the invention was termed TN70 and
CC was used as a template molecule for the PCR reaction. Primer p-s01 is
CC an oligonucleotide fragment in which a EaeI recognition site has
CC been introduced into its 5' end. The sequence is derived from the N-
CC terminal amino acid sequence, Thr-Val-Ala-Ala-Cys-Asn-Leu-Pro, of
CC TN70. p-a01 is an oligonucleotide fragment in which a BamHI
CC recognition sequence has been introduced into the 3' end. The
CC nucleotide sequence is derived from the C-terminal sequence of TN70,
CC Arg-Phe-Ser-Asn. This causes the C-terminus to become Asn from being
CC a stop codon.
XX
SQ Sequence 26 BP; 6 A; 4 C; 9 G; 7 T; 0 other;

Query Match 68.0%; Score 13.6; DB 13; Length 26;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ccatctgacattgggatcca 20
||| |||||| |||||||
Db 20 CCAACTGACAACTGGATCCA 1

RESULT 7
AAQ41891/c
ID AAQ41891 standard; DNA; 26 BP.
XX
AC AAQ41891;
XX
DT 16-SEP-1993 (first entry)
XX
DE Factor Xa inhibiting peptide BamHI primer.
XX
KW Factor Xa; inhibition; urinary trypsin inhibitor; Bikunin; elastase;
KW substitution; mutation; secretion; drug; UTI; infestation; shock;
KW pancreatitis; ischaemic heart disease; rheumatoid arthritis; ss.
XX
OS Synthetic.
XX
PN EP543240-A.
XX
PD 26-MAY-1993.
XX
PF 06-NOV-1992; 92EP-0119083.
XX
PR 08-NOV-1991; 91JP-0293472.
PR 12-MAY-1992; 92JP-0119289.
XX
PA (MOCH) MOCHIDA PHARM CO LTD.
XX
PI Kanamori T, Morishita H, Nobuhara M;
XX
DR WPI; 1993-168945/21.
XX
PT New polypeptide inhibiting protease(s), esp. FXa - used for
PT treating multiple organ failure, shock, pancreatitis,
PT disseminated intravascular coagulation, etc.
XX
PS Disclosure; Fig 7; 130pp; English.
XX
CC The sequences given in AAQ41889-903 are primers which were used in the
CC construction of plasmids encoding polypeptides which have factor Xa
CC inhibition activity. These peptides are based on a wild type sequence
CC which coincides with part of the amino acid sequence of urinary trypsin
CC inhibitor (UTI) or Bikunins (H1-30). It is different to both of these
CC proteins however, in its factor Xa inhibiting activity. Substitutions/
CC mutations of the wild type sequence may increase factor Xa inhibiting
CC activity, improve secretion of the polypeptide from the host cell or
CC increase the ability of the protein to inhibit other proteins, eg.
CC elastase. These properties may also be effected by supplementing one
CC or more amino acids at the C- and/or N-terminal of these proteins.
CC These peptides may be used in drug compositions for the prevention
CC and/or treatment of infestation, shock, pancreatitis, ischaemic heart
CC disease and rheumatoid arthritis.
XX
SQ Sequence 26 BP; 6 A; 4 C; 9 G; 7 T; 0 other;

Query Match 68.0%; Score 13.6; DB 14; Length 26;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ccatctgacattgggatcca 20
||| |||||| |||||||
Db 20 CCAACTGACAACTGGATCCA 1

RESULT 8
AAT36048
ID AAT36048 standard; cDNA; 25 BP.
XX
AC AAT36048;
XX
DT 19-NOV-1996 (first entry)
XX
DE Murine InK4D-p19 gene 3' primer.
XX
KW InK4D-p19; cyclin-dependent kinase inhibitor; CDK4; CDK6; cancer;
KW diagnosis; prognosis; gene therapy; antisense; transgenic animal;
KW polymerase chain reaction; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO9624603-A1.
XX
PD 15-AUG-1996.
XX
PF 06-FEB-1996; 96WO-US01643.
XX
PR 06-FEB-1995; 95US-0384106.
XX
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI Downing JR, Hirai H, Oduka T, Sherr CJ;
XX
DR WPI; 1996-384390/38.
XX
PT Inhibitors of cyclin-dependent kinase(s) CDK4 and CDK6 - useful to
PT arrest eukaryotic cell growth and determine oncogenic or
PT carcinogenic potential of a compsn.
XX
PS Example 2; Page 35; 86pp; English.
XX
CC A 5' PCR primer (AAT36047) contains a BamHI site and the 5' end
CC of the coding sequence (see also AAT36043) of novel murine InK4D-p19

```
CC   (AAW03744), an inhibitor of cyclin-dependent kinases CDK4 and CDK6.
CC   It was used with a 3' primer (AAT36048) to amplify the entire p19
CC   coding sequence.  Another primer pair (AAT36049-50) was used to
CC   amplify murine InKc-p18 cDNA (AAT36042).  PCR products were separately
CC   incorporated into vector pGEX-3X.  InKD-p19 and InKc-p18 were
CC   expressed as GST fusion proteins in Escherichia coli.
XX
SQ   Sequence 25 BP; 7 A; 7 C; 4 G; 7 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 17;  Length 25;
  Best Local Similarity   93.3%;  Pred. No. 7.3e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 tctgacattgggatc 18
           ||| ||||||||||||
Db       7 tctcacattgggatc 21


RESULT   9
AAT65534/c
ID   AAT65534 standard; DNA; 30 BP.
XX
AC   AAT65534;
XX
DT   14-SEP-1999  (first entry)
XX
DE   Oligonucleotide 123L-5' for chimeric protein construct.
XX
KW   Haematopoietic protein; human; granulocyte-colony stimulating factor;
KW   G-CSF; interleukin; c-mpl ligand; linker; gene therapy; aplastic anaemia;
KW   stem cell expansion; leukopaenia; neutropaenia; vector; bone marrow;
KW   thrombocytopaenia;  blood cell activation; growth; ss.
XX
OS   Synthetic.
XX
PN   WO9712985-A2.
XX
PD   10-APR-1997.
XX
PF   04-OCT-1996;   96WO-US15774.
XX
PR   05-OCT-1995;   95US-0004834.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Bauer SC,  Baum CM,  Caparon MH,  Feng Y,  Giri JG;
PI   Klein BK,  Lee SC,  McKearn JP,  McWherter CA,  Staten NR;
PI   Summers NL,  Zurfluh L;
XX
DR   WPI; 1997-226228/20.
XX
PT   Multi-functional haematopoietic receptor agonists - used to
PT   stimulate the production of haematopoietic cells in patients
XX
PS   Examples 8-44; Page 84; 616pp; English.
XX
CC   The invention relates to a novel haematopoietic protein (HP) comprising
CC   an amino acid (AA) sequence of formula: R1-L1-R2; R2-L1-R1; R1-R2; or
CC   R2-R1; where R1 and R2 are independently selected from: (I) a modified
CC   human granulocyte-colony stimulating factor (hG-CSF) AA sequence;
CC   (II) a modified human interleukin-3 (hIL-3) AA sequence; (III) a
CC   modified human c-mpl ligand; and a colony stimulating factor (CSF);
CC   and L1 = a linker capable of linking R1 to R2.  This sequence
CC   represents an oligonucleotide used to construct a gene encoding
CC   a protein of the invention.
CC   Vectors comprising the nucleic acid molecules are useful for the
CC   recombinant production of HP.  The nucleic acid molecules are useful in
CC   gene therapy.  The HP's are useful for stimulating the production of
CC   haematopoietic cells in patients, selective ex vivo expansion of stem
CC   cells and for treatment of haematopoietic disorders.  Disorders that
CC   can be treated include leukopaenia, neutropaenia, aplastic anaemia and
CC   thrombocytopaenia.  In vitro uses include the ability to stimulate bone
CC   marrow and blood cell activation and growth before infusion into the
CC   patients.
SQ   Sequence 30 BP; 6 A; 11 C; 5 G; 8 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 18;  Length 30;
  Best Local Similarity   93.3%;  Pred. No. 7.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       6 tgacattgggatcca 20
           || ||||||||||||
Db      22 TGGCATTGGGATCCA 8


RESULT  10
AAT63004/c
ID   AAT63004 standard; DNA; 30 BP.
XX
AC   AAT63004;
XX
DT   01-JAN-1998  (first entry)
XX
DE   c-mpl receptor agonist (123-153/5L/1-122) PCR primer 123-5'.
XX
KW   C-mpl ligand; thrombopoietin; receptor; agonist; cytokine; human;
KW   haematopoietic cell; stem cell; thrombocytopaenia; gene therapy;
KW   polymerase chain reaction; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9712978-A1.
XX
PD   10-APR-1997.
XX
PF   04-OCT-1996;   96WO-US15938.
XX
PR   05-OCT-1995;   95US-0004824.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Feng Y,  Giri JG,  McKearn JP,  McWherter CA,  Pegg LE;
PI   Staten NR,  Summers NL;
XX
DR   WPI; 1997-226221/20.
XX
PT   Novel c-mpl receptor agonist polypeptide(s) - stimulate
PT   haematopoietic cell production, useful in thrombocytopenia treatment
PT   and selective ex vivo expansion of haematopoietic stem cells
XX
PS   Example 7; Page 54; 151pp; English.
XX
CC   Forward primer 123-5' (AAT63004) and reverse primer 123-3' (AAT63005)
CC   were used in the generation of a synthetic gene (see AAT62972) coding
CC   for a novel, claimed c-mpl receptor agonist, 123-153/5L/1-122
CC   (see AAW15015).  The Horlick method was used with pMON28501 (see
CC   AAT62979), encoding c-mpl dimer, as template.  The PCR product was
CC   subcloned into a mammalian vector for expression in transfected BHK
CC   cells.  Specifically claimed circularly permuted variants of c-mpl
CC   ligand (see AAW15005-16) are useful in the treatment of
CC   thrombocytopaenia and selective ex vivo expansion of haematopoietic
CC   stem cells.
XX
SQ   Sequence 30 BP; 6 A; 11 C; 5 G; 8 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 18;  Length 30;
  Best Local Similarity   93.3%;  Pred. No. 7.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       6 tgacattgggatcca 20
           || ||||||||||||
Db      22 TGGCATTGGGATCCA 8
```

```
RESULT  11
AAV55446/c
ID   AAV55446 standard; DNA; 30 BP.
XX
AC   AAV55446;
XX
DT   24-NOV-1998  (first entry)
XX
DE   Primer 123-5' for c-mpl ligand.
XX
KW   Haematopoietic receptor agonist; human; c-mpl ligand;
KW   chimeric protein; stem cell expansion; tumour; infection;
KW   autoimmune disease; haematopoietic disorder; therapy;
KW   dendritic cell; PCR; primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO9817810-A2.
XX
PD   30-APR-1998.
XX
PF   23-OCT-1997;   97WO-US20037.
XX
PR   25-OCT-1996;   96US-0029629.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Feng Y,  McKearn JP,  McWherter CA,  Minnerly JC,  Minster NI;
PI   Staten NR,  Streeter PR,  Summers NL,  Woulfe SL;
XX
DR   WPI; 1998-261504/23.
XX
PT   Multi-functional chimeric haematopoietic receptor agonist - useful
PT   to treat haematopoietic disorders, tumours, infections or autoimmune
PT   diseases
XX
PS   Example 18; Page 93; 841pp; English.
XX
CC   Primers 123-5' and 123-3' (see AAV55447) are 5' and 3' primers,
CC   respectively for the c-mpl ligand gene sequence beginning at the
CC   codon corresponding to residue 123 of the native sequence.  They
CC   were used with PCR templates pMON28548, pMON28501, pMON28500 and
CC   pMON28502 (see AAV55114-17) to generate gene fragments (see AAV55162,
CC   AAV55174, AAV55186 and AAV55188) encoding sequence-rearranged c-mpl
CC   ligand polypeptides (see AAW77871, AAW77883, AAW77895 and AAW77897) that
CC   act as c-mpl receptor agonists. The invention relates to novel
CC   multi-functional chimeric haematopoietic receptor agonists (see
CC   AAW77780-822) that may include sequence-rearranged c-mpl ligand (see
CC   AAW77785).
XX
SQ   Sequence 30 BP; 6 A; 11 C; 5 G; 8 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 19;  Length 30;
  Best Local Similarity   93.3%;  Pred. No. 7.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       6 tgacattgggatcca 20
           || ||||||||||||
Db      22 TGGCATTGGGATCCA 8


RESULT  12
AAA10268
ID   AAA10268 standard; DNA; 43 BP.
XX
AC   AAA10268;
XX
DT   03-JUL-2000  (first entry)
XX
DE   PSMA monoclonal antibody VL region corrective PCR primer, VL backward.
XX
KW   Prostate-specific membrane antigen; PSMA; J591 hybridoma;
KW   monoclonal antibody; light chain variable region; VL;
KW   single chain variable region; scFv; single chain antibody;
KW   fusion receptor; T-cell receptor gamma-chain; immune response;
KW   prostate cancer; PCR primer; ss.
XX
OS   Unidentified.
XX
PN   WO200014257-A1.
XX
PD   16-MAR-2000.
XX
PF   03-SEP-1999;   99WO-US20349.
XX
PR   04-SEP-1998;   98US-0099138.
XX
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI   Sadelain M,  Bander NH,  Gong M;
XX
DR   WPI; 2000-257002/22.
XX
PT   A fusion receptor composition having the structure:prostate-specific
PT   membrane antigen-single chain variable fragment:optional
PT   connector:cytoplasmic domain, useful for treatment of cancer -
XX
PS   Example 1; Page 10; 25pp; English.
XX
CC   The invention relates to a novel fusion receptor composition having the
CC   structure: PSMA (prostate-specific membrane antigen)-scFv (single chain
CC   variable fragment):optional connector:cytoplasmic domain, where the
CC   fusion receptor is effective when expressed in a T-cell to promote a
CC   cellular immune response to PSMA. The PSMA-scFv is a single-chain
CC   antibody cloned from the V region genes of a hybridoma specific for
CC   PSMA, such as J591. The optional connector is provided to give a spacing
CC   between the PSMA-scFv and the cytoplasmic domain, such that both retain
CC   substantial function. The cytoplasmic domain directs the function of the
CC   fusion receptor and is generally the cytoplasmic domain of a molecule
CC   which functions as a transducer of a mammalian immune response in the
CC   presence of an MHC (major histocompatibility complex)-peptide complex or
CC   costimulatory factor. Examples of cytoplasmic domains that may be
CC   employed in the present invention include the T-cell receptor
CC   gamma-chain cytoplasmic domain and the CD28 cytoplasmic domain. In a
CC   method of the invention, an expression vector encoding the fusion
CC   receptor is transduced into primary T-lymphocytes obtained from the
CC   patient to be treated. The transduced lymphocytes are returned to the
CC   patient where they secrete interleukin-2 (IL-2) and proliferate in
CC   response to PSMA- positive cells. The resulting cytotoxic lymphocytes
CC   specifically lyse cells expressing PSMA and can thus be used to target
CC   PSMA-positive tumour cells. The fusion receptor promotes a cellular
CC   immune response to PSMA and is useful for the treatment of prostate
CC   cancer and other cancers that express PSMA. Sequences AAA10266-A10269
CC   represent PCR primers used in an exemplification of the present invention
CC   to amplify and correct cDNA encoding the VL region of a PMSA monoclonal
CC   antibody. Sequences AAA10266- AAA10267 represent reverse
CC   transcriptase-PCR (RT-PCR) primers used to amplify VL cDNA from the J591
CC   hybridoma cell line, and primers AAA10268- AAA10269 were used in a second
CC   round of PCR to correct the amplified sequence. The VL DNA was used for
CC   the construction of a gene encoding a PSMA-specific single chain
CC   antibody, which in turn was used to construct a gene encoding a fusion
CC   receptor comprising the PSMA-scFv, a CD8 hinge and transmembrane region,
CC   and a T-cell receptor gamma-chain.
XX
SQ   Sequence 43 BP; 15 A; 8 C; 9 G; 11 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 21;  Length 43;
  Best Local Similarity   93.3%;  Pred. No. 7.9e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       3 atctgacattgggat 17
           ||||||||||| |||
```

```
Db      8 atctgacattgtgat 22


RESULT  13
AAF90190/c
ID   AAF90190 standard; DNA; 36 BP.
XX
AC   AAF90190;
XX
DT   06-AUG-2001  (first entry)
XX
DE   PCR primer for DNA encoding the amino terminal of flagellin.
XX
KW   Flagellin; gram-negative bacteria; peritonitis; pneumonia; bacteremia;
KW   sepsis; cystitis; urethritis; meningitis; osteomylitis; encephalitis;
KW   wound infection; burn; gingivitis; otitis media; tonsillitis; typhilitis;
KW   PCR primer; ss.
XX
OS   Salmonella muenchen.
XX
PN   WO200140280-A2.
XX
PD   07-JUN-2001.
XX
PF   29-NOV-2000; 2000WO-US42381.
XX
PR   29-NOV-1999;   99US-0167801.
PR   28-NOV-2000; 2000US-0167801.
XX
PA   (INOT-) INOTEK CORP.
XX
PI   Salzman AL,  Murthy K,  Szabo C;
XX
DR   WPI; 2001-367805/38.
XX
PT   New purified flagellin polypeptide derived from amino terminal region
PT   of bacterial flagellin polypeptide, useful for neutralizing gram
PT   negative bacterial infection such as meningitis, sepsis and pneumonia
PT   in humans  -
XX
PS   Example 1; Page 28; 41pp; English.
XX
CC   PCR primers AAF90190-91 were used to amplify DNA encoding the amino
CC   terminal of flagellin. The polypeptide fragment has an epitope that binds
CC   to an antibody that neutralizes a gram-negative bacterial infection.
CC   Flagellin fragments, and antibodies that bind them, are useful for
CC   preventing an infection associated with a gram negative bacterium in a
CC   mammal. They are also useful for treating gram negative bacterial
CC   infection such as peritonitis, pneumonia, bacteremia, sepsis, cystitis,
CC   urethritis, meningitis, osteomylitis, encephalitis, wound infection,
CC   burns, gingivitis, otitis media, tonsillitis, typhilitis etc., in a
CC   subject, caused by gram negative pathogens such as Salmonella spp.,
CC   Aeromonas spp., Yersinia spp., Proteus spp., Serratia spp., Pseudomonas
CC   spp., or Vibrio spp..
XX
SQ   Sequence 36 BP; 14 A; 10 C; 6 G; 6 T; 0 other;


  Query Match             66.0%;  Score 13.2;  DB 22;  Length 36;
  Best Local Similarity   83.3%;  Pred. No. 9.8e+02;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2 catctgacattgggatcc 19
           | | ||  ||||||||||
Db      21 CTTGTGCCATTGGGATCC 4


RESULT  14
AAT37559/c
ID   AAT37559 standard; mRNA; 15 BP.
XX
AC   AAT37559;
XX
DT   11-NOV-1996  (first entry)
XX
DE   Apo(a) mRNA (nt. pos. 11266) hammerhead ribozyme target sequence.
XX
KW   Enzymatic RNA molecule; cleavage; apolipoprotein (a); apo(a);
KW   hammerhead ribozyme; target sequence; diagnosis; treatment;
KW   lipoprotein (a); atherosclerosis; myocardial infarction; stroke;
KW   restenosis; heart disease; human; ss.
XX
OS   Homo sapiens.
XX
PN   WO9609392-A1.
XX
PD   28-MAR-1996.
XX
PF   21-SEP-1995;   95WO-US11995.
XX
PR   23-SEP-1994;   94US-0311760.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   McSwiggen J,  Newton RS,  Ramharack R,  Stinchcomb DT;
XX
DR   WPI; 1996-188454/19.
XX
PT   Enzymatic RNA mols. which cleave apo(a) mRNA - useful in diagnosis
PT   and treatment of conditions related to Lp(a) levels, e.g.
PT   atherosclerosis, myocardial infarction, and heart diseases
XX
PS   Claim 2; Page 18; 37pp; English.
XX
CC   A claimed enzymatic RNA mol. for the cleavage of apolipoprotein (a)
CC   (apo(a)) mRNA, specifically a hammerhead ribozyme, has binding arms
CC   complementary to the present sequence (nucleotide position 11266).
CC   The ribozyme blocks to some extent apo(a) expression, and can
CC   therefore be used to diagnose or treat conditions related to
CC   lipoprotein (a) levels, e.g. atherosclerosis, myocardial
CC   infarction, stroke, restenosis and heart disease.
CC   PCR was used to generate a substrate for T7 RNA polymerase
CC   transcription from human apo(a) cDNA clones. Labelled transcripts
CC   were synthesised in vitro to form 2 templates. The oligonucleotides
CC   and labelled transcripts were annealed, RNaseH added and the mixts.
CC   incubated. After a designated time the reactions were stopped, and
CC   RNA sepd. on sequencing polyacrylamide gels. The percentage of
CC   substrate cleaved was determined by autoradiographic
CC   quantification, and the most accessible ribozyme target sites
CC   chosen.
XX
SQ   Sequence 15 BP; 4 A; 4 C; 3 G; 4 U; 0 other;


  Query Match             65.0%;  Score 13;  DB 17;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       8 acattgggatcca 20
           |||||||||||||
Db      15 ACATTGGGATCCA 3


RESULT  15
AAZ74940/c
ID   AAZ74940 standard; DNA; 18 BP.
XX
AC   AAZ74940;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human biallelic marker downstream amplification primer SEQ ID NO:9296.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
```

KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 8; Page 2212; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 other;

Query Match 64.0%; Score 12.8; DB 21; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ccatctgacattggga 16
|||| |||||||| ||
Db 17 CCATGTGACATTGTGA 2

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Job time: 5155 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 09:50:31 ; Search time 1263.07 Seconds
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Title: US-09-923-515-17
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15	75.0	15	17	AAT37560	Apo(a) mRNA (nt. p
c	2	14.2	71.0	28	19	AAV64594	Human native inter
	3	13.6	68.0	20	20	AAX92916	PCR primer used to
c	4	13.4	67.0	20	19	AAV23052	HG5647S-20 primer
c	5	13.4	67.0	53	21	AAC70054	VEGF-binding nucle
	6	13	65.0	51	21	AAA77044	Human clone cg4332
	7	13	65.0	51	21	AAA77045	Human clone cg4332
	8	12.8	64.0	36	22	AAF60063	Primer NOOL-9. Sy
	9	12.8	64.0	40	22	AAC88050	PCR amplification
	10	12.6	63.0	21	21	AAC84008	Antisense oligonuc
c	11	12.6	63.0	28	19	AAV64595	Human native inter
c	12	12.6	63.0	31	22	AAI30310	Human single nucle
	13	12.6	63.0	36	21	AAA73246	Consensus phytase
	14	12.6	63.0	36	21	AAZ59653	Phytase-1 K91A mut
c	15	12.6	63.0	36	21	AAZ59654	Phytase-1 K91A mut
	16	12.6	63.0	36	22	AAS05732	Site directed muta
c	17	12.6	63.0	36	22	AAS05733	Site directed muta
c	18	12.6	63.0	37	17	AAT17826	Primer #13 for sec
c	19	12.6	63.0	51	22	AAH89265	Human coding sequ
	20	12.4	62.0	20	13	AAQ32826	Microsatellite rep
	21	12.4	62.0	20	15	AAQ57849	Primer pair 19A HS
	22	12.4	62.0	20	18	AAT94357	Human DPC4 sequenc
c	23	12.4	62.0	51	21	AAA76588	Human clone cg2142
c	24	12.4	62.0	51	21	AAA76589	Human clone cg2142
	25	12.4	62.0	60	18	AAT92161	Human DPC4 in vitr
c	26	12.2	61.0	20	17	AAT39491	Steroidogenesis ac
c	27	12.2	61.0	22	21	AAA35410	Myrtaceae microsat
c	28	12.2	61.0	27	19	AAV93995	Human IL-2 recepto
c	29	12.2	61.0	28	19	AAV40721	Primer for aldehyd
	30	12.2	61.0	30	19	AAV73293	PCR primer 2. Syn
	31	12.2	61.0	30	20	AAX04777	PCR primer of the
c	32	12.2	61.0	32	21	AAZ43235	PCR primer for C.
	33	12.2	61.0	36	19	AAV73297	PCR primer L3PSTNO
	34	12.2	61.0	37	22	AAF89670	Probe used to iden
	35	12.2	61.0	38	21	AAA90380	Human angiostatin
	36	12.2	61.0	38	21	AAA56863	Reverse primer for
	37	12.2	61.0	38	21	AAZ58999	Human angiostatin
	38	12.2	61.0	38	22	AAH96857	Human Chk1 ribozym
c	39	12.2	61.0	45	16	AAQ95046	Human hippocampal
	40	12.2	61.0	47	21	AAZ69349	Human map-related
c	41	12.2	61.0	60	21	AAZ29388	PCR primer-14 for
	42	12	60.0	15	22	AAF69554	Human IL4Ralpha ge
	43	12	60.0	15	22	AAF69556	Human IL4Ralpha ge
c	44	12	60.0	19	21	AAA29708	CC49 heavy chain o
c	45	12	60.0	19	21	AAZ40729	Primer 2 for seque

ALIGNMENTS

RESULT 1
AAT37560/c
ID AAT37560 standard; mRNA; 15 BP.
XX
AC AAT37560;
XX
DT 11-NOV-1996 (first entry)
XX
DE Apo(a) mRNA (nt. pos. 362) hammerhead ribozyme target sequence.
XX
KW Enzymatic RNA molecule; cleavage; apolipoprotein (a); apo(a);
KW hammerhead ribozyme; target sequence; diagnosis; treatment;
KW lipoprotein (a); atherosclerosis; myocardial infarction; stroke;
KW restenosis; heart disease; human; ss.
XX
OS Homo sapiens.
XX
PN WO9609392-A1.
XX
PD 28-MAR-1996.
XX
PF 21-SEP-1995; 95WO-US11995.
XX
PR 23-SEP-1994; 94US-0311760.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI McSwiggen J, Newton RS, Ramharack R, Stinchcomb DT;
XX
DR WPI; 1996-188454/19.
XX
PT Enzymatic RNA mols. which cleave apo(a) mRNA - useful in diagnosis
PT and treatment of conditions related to Lp(a) levels, e.g.
PT atherosclerosis, myocardial infarction, and heart diseases

XX
PS Claim 2; Page 18; 37pp; English.
XX
CC A claimed enzymatic RNA mol. for the cleavage of apolipoprotein (a)
CC (apo(a)) mRNA, specifically a hammerhead ribozyme, has binding arms
CC complementary to the present sequence (nucleotide position 362).
CC The ribozyme blocks to some extent apo(a) expression, and can
CC therefore be used to diagnose or treat conditions related to
CC lipoprotein (a) levels, e.g. atherosclerosis, myocardial
CC infarction, stroke, restenosis and heart disease.
CC PCR was used to generate a substrate for T7 RNA polymerase
CC transcription from human apo(a) cDNA clones. Labelled transcripts
CC were synthesised in vitro to form 2 templates. The oligonucleotides
CC and labelled transcripts were annealed, RNaseH added and the mixts.
CC incubated. After a designated time the reactions were stopped, and
CC RNA sepd. on sequencing polyacrylamide gels. The percentage of
CC substrate cleaved was determined by autoradiographic
CC quantification, and the most accessible ribozyme target sites
CC chosen.
XX
SQ Sequence 15 BP; 5 A; 5 C; 3 G; 2 U; 0 other;

Query Match 75.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 tgcgtctgagcattg 18
||||||||||||||||
Db 15 TGCGTCTGAGCATTG 1

RESULT 2
AAV64594/c
ID AAV64594 standard; DNA; 28 BP.
XX
AC AAV64594;
XX
DT 29-JAN-1999 (first entry)
XX
DE Human native interferon-beta primer F15/C17.
XX
KW Interferon-Beta; variant; human; medicament; treatment; screening;
KW multiple sclerosis; measurement; water soluble; primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN DE19717864-A1.
XX
PD 29-OCT-1998.
XX
PF 23-APR-1997; 97DE-1017864.
XX
PR 23-APR-1997; 97DE-1017864.
XX
PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX
PI Otto B, Schneider-Fresenius C, Waschuetza G;
XX
DR WPI; 1998-569784/49.
XX
PT New mutated recombinant human interferon-beta protein contains
PT hydroxylic amino acid substitutions to improve water solubility -
PT used e.g. in in vitro screening assays, to measure interferon levels
PT and to treat multiple sclerosis
XX
PS Disclosure; Fig 4; 18pp; German.
XX
CC AAV64592-V64610 are primers used in the construction of a mutant human
CC recombinant interferon-beta in which an amino acid having at least one
CC hydroxy group is substituted for at least one of Leu5, Phe8, Phe15,
CC Leu47, Phe50, Leu106, Phe111, Leu116, Leu120 and Phe156. Such mutants
CC can be used in medicaments e.g. for treating multiple sclerosis, for in
CC vitro screening assays and for measurement of interferon levels. The
CC mutated protein is more water-soluble than recombinant wild-type human
CC interferon-beta.
XX
SQ Sequence 28 BP; 8 A; 10 C; 5 G; 5 T; 0 other;

Query Match 71.0%; Score 14.2; DB 19; Length 28;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ttctgcgtctgagcattgc 19
||||| | ||||| |||||
Db 23 TTCTGGGACTGAGAATTGC 5

RESULT 3
AAX92916
ID AAX92916 standard; DNA; 20 BP.
XX
AC AAX92916;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydia pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB01890.
XX
PR 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae
XX
PS Page 1549; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading
CC frames and other nucleic acid sequences from the genome of
CC Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory
CC disease such as pneumonia and bronchitis and is thought to be a
CC contributing factor in heart disease, sarcoidosis, sinusitis, purulent
CC otitis media, erythema nodosum or pharyngitis. The polypeptides encoded
CC by the open reading frames of the C. pneumoniae genome (see AAY34584-
CC AAY35879) can be used in immunogenic compositions as vaccines. Vectors
CC containing C. pneumoniae nucleotides sequences can also be used as
CC immunogenic compositions, especially where the vector directs the
CC expression of a neutralising epitope of C. pneumoniae.
XX
SQ Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 other;

Query Match 68.0%; Score 13.6; DB 20; Length 20;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ttctgcgtctgagcattgcg 20

```
          || ||| ||||| | |||||
Db      1 ttatgcctctgatccttgcg 20


RESULT   4
AAV23052/c
ID   AAV23052 standard; DNA; 20 BP.
XX
AC   AAV23052;
XX
DT   30-JUL-1998  (first entry)
XX
DE   HG5647S-20 primer used to amplify Hepatitis virus g gene sequences.
XX
KW   Hepatitis g virus gene; diagnosis; treatment; Hepatitis g virus disease;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Hepatitis g virus.
XX
PN   JP10108685-A.
XX
PD   28-APR-1998.
XX
PF   10-AUG-1997;   97JP-0227387.
XX
PR   10-AUG-1996;   96JP-0227639.
XX
PA   (BMLB-) BML KK.
XX
DR   WPI; 1998-304974/27.
XX
PT   New hepatitis G virus gene - useful for diagnosing and treating
PT   diseases caused by virus
XX
PS   Disclosure; Page 6; 128pp; Japanese.
XX
CC   PCR primers AAV23018-74 were used to amplify and isolate new Hepatitis g
CC   virus gene (see AAV23075-83 for gene fragments). RNA was synthesised
CC   from the serum of nine patients judged positive for Hepatitis g virus
CC   and cDNA synthesised from this RNA. The cDNA was used as a template in
CC   several PCR reactions to isolate fragments of the new gene. The gene
CC   may be useful for diagnosing and developing treatments for Hepatitis g
CC   virus diseases.
XX
SQ   Sequence 20 BP; 5 A; 6 C; 8 G; 1 T; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 19;  Length 20;
  Best Local Similarity   93.3%;  Pred. No. 8.4e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       5 gcgtctgagcattgc 19
           ||||||||||  ||||
Db      19 GCGTCTGAGCGTTGC 5


RESULT   5
AAC70054/c
ID   AAC70054 standard; RNA; 53 BP.
XX
AC   AAC70054;
XX
DT   30-JAN-2001  (first entry)
XX
DE   VEGF-binding nucleic acid ligand identified by SELEX, SEQ ID NO:249.
XX
KW   SELEX; systematic evolution of ligands by exponential enrichment;
KW   nucleic acid ligand; aptamer; in vitro evolution; iterative selection;
KW   human VEGF-binding; vascular endothelial growth factor; ss.
XX
OS   Synthetic.
XX
PN   WO200056930-A1.
XX
PD   28-SEP-2000.
XX
PF   20-MAR-2000; 2000WO-US07486.
XX
PR   24-MAR-1999;   99US-0275850.
XX
PA   (NEXS-) NEXSTAR PHARM INC.
XX
PI   Pagratis N,  Gold L,  Shtatland T,  Javornik B;
XX
DR   WPI; 2000-594583/56.
XX
PT   Identifying nucleic acid ligands of a target molecule comprises
PT   annealing complementary oligonucleotides, partitioning the nucleic
PT   acids and amplifying the nucleic acids exhibiting increased affinity -
XX
PS   Example 9; Page 226; 264pp; English.
XX
CC   The invention relates to a method of identifying nucleic acid ligands of
CC   a target molecule from a candidate mixture composed of single stranded
CC   nucleic acids, each having a region of randomised sequence and a region
CC   of fixed sequence. The method uses modified versions of the SELEX
CC   (systematic evolution of ligands by exponential enrichment) method in
CC   which the participation of fixed sequences is minimised or eliminated.
CC   This method comprises annealing complementary oligonucleotides to the
CC   fixed sequences of the candidate molecule mixture, contacting the
CC   candidate mixture with the target molecule, partitioning the nucleic
CC   acids which have increased affinity relative to the candidate mixture,
CC   and amplifying the nucleic acids exhibiting increased affinity to yield
CC   a ligand enriched mixture of nucleic acids. In one embodiment of the
CC   invention, one or more regions of fixed sequences is replaced with
CC   different fixed sequences, and the binding, partitioning and
CC   amplification steps are repeated. In another embodiment, the partitioned
CC   nucleic acids are hybridised with a library of single stranded
CC   complementary nucleic acids, are then amplified, and the fixed regions
CC   of the increased affinity nucleic acids cleaved. The present sequence
CC   represents a nucleic acid ligand capable of binding to human VEGF
CC   (vascular endothelial growth factor) which was identified using a SELEX
CC   method of the invention.
XX
SQ   Sequence 53 BP; 11 A; 12 C; 18 G; 12 U; 0 other;


  Query Match             67.0%;  Score 13.4;  DB 21;  Length 53;
  Best Local Similarity   93.3%;  Pred. No. 9.5e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       6 cgtctgagcattgcg 20
           ||||||||||| |||
Db      43 CGTCTGAGCATAGCG 29


RESULT   6
AAA77044
ID   AAA77044 standard; cDNA; 51 BP.
XX
AC   AAA77044;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Human clone cg43328092 polymorphic site, SEQ ID NO:727.
XX
KW   Human; single nucleotide polymorphism; SNP; chromosome 8;
KW   detection; identification; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace (26,G)
FT                   /*tag= a
XX
```

PN WO200029623-A2.
XX
PD 25-MAY-2000.
XX
PF 17-NOV-1999; 99WO-US27293.
XX
PR 17-NOV-1998; 98US-0109024.
PR 16-NOV-1999; 99US-0109024.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2000-387826/33.
XX
PT Human nucleic acids containing single nucleotide polymorphisms, useful
PT for treating a subject suffering, or at risk from a pathology due to
PT the presence of a sequence polymorphism -
XX
PS Claim 1; Page 377; 543pp; English.
XX
CC Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC 1112 (AAA76318-A77429) are consecutive pairs of nucleotides which
CC contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
CC consecutive pairs of nucleotides containing SNPs which result in changes
CC in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC in non- conservative changes. The SNPs in sequences 1187 to 1192
CC (AAA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals.
XX
SQ Sequence 51 BP; 12 A; 10 C; 14 G; 15 T; 0 other;

Query Match 65.0%; Score 13; DB 21; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 tctgcgtctgagc 14
||||||||||||||
Db 39 tctgcgtctgagc 51

RESULT 7
AAA77045
ID AAA77045 standard; cDNA; 51 BP.
XX
AC AAA77045;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human clone cg43328092 polymorphic site, SEQ ID NO:728.
XX
KW Human; single nucleotide polymorphism; SNP; chromosome 8;
KW detection; identification; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace (26,A)
FT /*tag= a
XX

PN WO200029623-A2.
XX
PD 25-MAY-2000.
XX
PF 17-NOV-1999; 99WO-US27293.
XX
PR 17-NOV-1998; 98US-0109024.
PR 16-NOV-1999; 99US-0109024.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2000-387826/33.
XX
PT Human nucleic acids containing single nucleotide polymorphisms, useful
PT for treating a subject suffering, or at risk from a pathology due to
PT the presence of a sequence polymorphism -
XX
PS Claim 1; Page 377; 543pp; English.
XX
CC Sequences AAA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC 1112 (AAA76318-A77429) are consecutive pairs of nucleotides which
CC contain silent SNPs. Sequences 1113 to 1192 (AAA77430-A77509) are
CC consecutive pairs of nucleotides containing SNPs which result in changes
CC in the corresponding amino acid sequences (AAB11749-B11828). The SNPs in
CC sequences 1113 to 1128 (AAA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AAA77446-A77503) result
CC in non- conservative changes. The SNPs in sequences 1187 to 1192
CC (AAA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals.
XX
SQ Sequence 51 BP; 11 A; 10 C; 15 G; 15 T; 0 other;

Query Match 65.0%; Score 13; DB 21; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 tctgcgtctgagc 14
||||||||||||||
Db 39 tctgcgtctgagc 51

RESULT 8
AAF60063
ID AAF60063 standard; DNA; 36 BP.
XX
AC AAF60063;
XX
DT 27-APR-2001 (first entry)
XX
DE Primer NOOL-9.
XX
KW Primer; selection; drug; vaccine; bioseparation; ss.
XX
OS Synthetic.
XX
PN WO200105808-A2.
XX
PD 25-JAN-2001.
XX
PF 20-JUL-2000; 2000WO-GB02809.

XX
PR 20-JUL-1999; 99GB-0017027.
XX
PA (AFFI-) AFFIBODY TECHNOLOGY SWEDEN AB.
PA (GARD/) GARDNER R.
XX
PI Nygren P, Uhlen M, Nord O;
XX
DR WPI; 2001-147323/15.
XX
PT In vitro selection of desired polypeptides for use as drug and in
PT vaccine development, by immobilizing nucleic acid molecule on solid
PT support carrying target for biospecific interaction with the desired
PT polypeptide -
XX
PS Disclosure; Page 24; 63pp; English.
XX
CC The present invention relates to a method of selecting one or
CC more desired polypeptides using a cell free expression of nucleic
CC acid molecules immobilized on a solid support system carrying
CC target for biospecific interaction with the desired peptide or
CC a molecule attached to it, to produce the polypeptide. The
CC solid support carrying both the desired polypeptide and nucleic acid
CC encoding it, is separated. The method is useful for selection and
CC identification of proteins or peptides with desired properties from
CC pools of protein or peptide variants. The polypeptides with desired
CC properties such as binding affinity to a particular target molecule,
CC catalytic activity, chemical or enzymatic activity or immunogenic
CC activity are useful as drugs, for vaccine development and in
CC diagnosis and bioseparation.
XX
SQ Sequence 36 BP; 7 A; 7 C; 10 G; 12 T; 0 other;

Query Match 64.0%; Score 12.8; DB 22; Length 36;
Best Local Similarity 87.5%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ttctgcgtctgagcat 16
||| ||| ||||||||
Db 18 ttcggcgcctgagcat 33

RESULT 9
AAC88050
ID AAC88050 standard; DNA; 40 BP.
XX
AC AAC88050;
XX
DT 09-MAR-2001 (first entry)
XX
DE PCR amplification oligonucleotide primer SNAP-4.
XX
KW Staphylococcal; protein A; self-assembling biomolecular structure;
KW anti-Staphylococcal protein A affibody affinity module; diagnosis;
KW affinity module; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200069888-A1.
XX
PD 23-NOV-2000.
XX
PF 15-MAY-2000; 2000WO-GB01843.
XX
PR 14-MAY-1999; 99GB-0011287.
XX
PA (AFFI-) AFFIBODY TECHNOLOGY SWEDEN AB.
PA (GARD/) GARDNER R.
XX
PI Nygren P, Uhlen M;
XX
DR WPI; 2001-025000/03.
XX
PT Self-assembled biomolecular structure used in therapy and ex vivo
PT diagnostic methods, comprises affinity modules having affinity domains,
PT which are capable of biospecific interaction to form assembled
PT structures -
XX
PS Example; Page 19; 41pp; English.
XX
CC The present invention describes a self-assembled biomolecular structure
CC (I) comprising affinity modules (AM) each of which has two similar or
CC different affinity domains (AD), and at least one AD within each AM has
CC specific and exclusive affinity for an AD within another AM. The AMs are
CC capable of biospecific interaction to form an assembled structure. (I)
CC is used in therapy and in an ex vivo diagnostic method. (I) may be
CC useful as materials, e.g. for encapsulation of active agents, or they
CC may have a more active functional role, e.g. in bioelectronic
CC applications. (I) has diagnostic applications, e.g. to obtain highly
CC avid reagents or clinical applications, e.g. to obtain controlled
CC delivery of therapeutics, nano-fabrication applications, e.g. to obtain
CC spontaneous build up of ordered small-scale structures, biotechnological
CC applications, e.g. to obtain thermally or chemically reversible protein
CC networks, and provision of basis for stepwise enzymatic treatment of a
CC substrate at a defined position. In clinical applications, enzymes or
CC therapeutics (including vaccines) may be encapsulated in self-assembling
CC biomolecular structures by mixing the affinity modules with the
CC substance to be encapsulated. The present sequence represents a PCR
CC primer which is used in the exemplification of the present invention.
XX
SQ Sequence 40 BP; 6 A; 12 C; 12 G; 10 T; 0 other;

Query Match 64.0%; Score 12.8; DB 22; Length 40;
Best Local Similarity 87.5%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ttctgcgtctgagcat 16
||| ||| ||||||||
Db 22 ttcggcgcctgagcat 37

RESULT 10
AAC84008
ID AAC84008 standard; DNA; 21 BP.
XX
AC AAC84008;
XX
DT 02-MAR-2001 (first entry)
XX
DE Antisense oligonucleotide #2 for inducible nitric oxide synthase gene.
XX
KW Vasotropic; gene therapy; antisense; inducible nitric oxide synthase;
KW iNOS; medicament; cerebral ischaemia; ss.
XX
OS Rattus sp.
XX
PN WO200066725-A1.
XX
PD 09-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-FR01191.
XX
PR 04-MAY-1999; 99FR-0005629.
PR 18-JUN-1999; 99US-0139735.
XX
PA (AVET) AVENTIS PHARMA SA.
XX
PI Parmentier S, Bohme A, Plotkine M;
XX
DR WPI; 2000-679758/66.
XX
PT Antisense oligonucleotides of an inductible isoform of nitrogen
PT monoxide synthase, used to treat cerebral ischemia -
XX

```
PS   Claim 4; Page 29; 35pp; French.
XX
CC   The invention relates to the use of antisense oligonucleotides to an
CC   inducible isoform of nitric oxide synthase (iNOS), for the preparation
CC   of a medicament to treat cerebral ischaemia. The oligonucleotides
CC   AAC84007-C84008 represent examples of the antisense oligonucleotides
CC   used in the invention.
XX
SQ   Sequence 21 BP; 3 A; 7 C; 4 G; 7 T; 0 other;


  Query Match            63.0%;  Score 12.6;  DB 21;  Length 21;
  Best Local Similarity  78.9%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ttctgcgtctgagcattgc 19
          ||| | |||||  ||||||
Db      2 ttcagagtctgcccattgc 20


RESULT  11
AAV64595/c
ID   AAV64595 standard; DNA; 28 BP.
XX
AC   AAV64595;
XX
DT   29-JAN-1999  (first entry)
XX
DE   Human native interferon-beta primer C17.
XX
KW   Interferon-Beta; variant; human; medicament; treatment; screening;
KW   multiple sclerosis; measurement; water soluble; primer; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   DE19717864-A1.
XX
PD   29-OCT-1998.
XX
PF   23-APR-1997;   97DE-1017864.
XX
PR   23-APR-1997;   97DE-1017864.
XX
PA   (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
XX
PI   Otto B,  Schneider-Fresenius C,  Waschuetza G;
XX
DR   WPI; 1998-569784/49.
XX
PT   New mutated recombinant human interferon-beta protein contains
PT   hydroxylic amino acid substitutions to improve water solubility -
PT   used e.g. in in vitro screening assays, to measure interferon levels
PT   and to treat multiple sclerosis
XX
PS   Disclosure; Fig 4; 18pp; German.
XX
CC   AAV64592-V64610 are primers used in the construction of a mutant human
CC   recombinant interferon-beta in which an amino acid having at least one
CC   hydroxy group is substituted for at least one of Leu5, Phe8, Phe15,
CC   Leu47, Phe50, Leu106, Phe111, Leu116, Leu120 and Phe156. Such mutants
CC   can be used in medicaments e.g. for treating multiple sclerosis, for in
CC   vitro screening assays and for measurement of interferon levels. The
CC   mutated protein is more water-soluble than recombinant wild-type human
CC   interferon-beta.
XX
SQ   Sequence 28 BP; 8 A; 9 C; 5 G; 6 T; 0 other;


  Query Match            63.0%;  Score 12.6;  DB 19;  Length 28;
  Best Local Similarity  78.9%;  Pred. No. 2.2e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ttctgcgtctgagcattgc 19
          ||||| | ||||  |||||
Db     23 TTCTGGGACTGAAAATTGC 5


RESULT  12
AAI30310/c
ID   AAI30310 standard; DNA; 31 BP.
XX
AC   AAI30310;
XX
DT   18-OCT-2001  (first entry)
XX
DE   Human single nucleotide polymorphism (SNP) LTB 2.
XX
KW   Human; resequence; genotype; disease; forensic; paternity testing;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Variation       replace(16,A)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO200166800-A2.
XX
PD   13-SEP-2001.
XX
PF   07-MAR-2001; 2001WO-US07268.
XX
PR   07-MAR-2000; 2000US-0187510.
PR   22-MAY-2000; 2000US-0206129.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Cargill M,  Ireland JS,  Lander ES;
XX
DR   WPI; 2001-522952/57.
XX
PT   Nucleic acid molecules from the human genome which include polymorphic
PT   sites, useful in methods for predicting the presence, absence or
PT   severity of a particular phenotype or disorder (e.g. diabetes)
PT   associated with a particular genotype -
XX
PS   Claim 1; Page 78; 145pp; English.
XX
CC   The invention relates to the identification of nucleic acid molecules
CC   (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC   which can predispose individuals to disease. Various genes from a number
CC   of individuals were resequenced and single nucleotide polymorphisms
CC   (SNPs) in these genes discovered. The method is useful for predicting the
CC   presence, absence or severity of a particular phenotype or disorder (e.g.
CC   diabetes) associated with a particular genotype. The nucleic acids
CC   containing the polymorphic sites may be useful in forensics and paternity
CC   testing.
XX
SQ   Sequence 31 BP; 3 A; 10 C; 13 G; 5 T; 0 other;


  Query Match            63.0%;  Score 12.6;  DB 22;  Length 31;
  Best Local Similarity  78.9%;  Pred. No. 2.3e+03;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 tctgcgtctgagcattgcg 20
          || ||||| ||| | ||||
Db     19 TCGGCGTCCGAGAACTGCG 1


RESULT  13
AAA73246
ID   AAA73246 standard; DNA; 36 BP.
XX
```

AC AAA73246;
XX
DT 05-DEC-2000 (first entry)
XX
DE Consensus phytase site-directed mutagenesis primer SEQ ID NO:46.
XX
KW Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW temperature stability; pH profile; temperature profile; reaction rate;
KW specific activity; substrate specificity; substrate cleavage pattern;
KW substrate binding; position specificity; phytate degradation rate;
KW food; feed; phytate; manure; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200043503-A1.
XX
PD 27-JUL-2000.
XX
PF 21-JAN-2000; 2000WO-DK00025.
XX
PR 22-JAN-1999; 99DK-0000092.
PR 21-SEP-1999; 99DK-0001340.
XX
PA (NOVO) NOVO NORDISK AS.
XX
PI Lehmann M;
XX
DR WPI; 2000-491161/43.
XX
PT Novel phytases with improved properties such as temperature stability,
PT pH stability and substrate specificity, for use in pharmaceuticals and
PT compound foods and feeds -
XX
PS Example 3; Page 38; 240pp; English.
XX
CC The present invention describes improved phytases, preferably with
CC increased thermostability, and methods for producing them. The methods
CC can be used for producing phytases with improved properties e.g.
CC temperature stability, pH stability, pH profile, temperature profile,
CC specific activity, substrate specificity, substrate cleavage pattern,
CC substrate binding, position specificity, the velocity and level of
CC release of phosphate from corn, reaction rate, phytate degradation rate,
CC and end level of released phosphate. The phytases can be used to produce
CC pharmaceutical compositions or compound food or feeds. The feed can be
CC used to reduce levels of phytate in animal manure, by converting it
CC into lower inositol phosphates and/or inositol and inorganic phosphate.
CC AAA73237 to AAA73289 represent phytase PCR primers and site-directed
CC mutagenesis primers used in examples from the present invention.
XX
SQ Sequence 36 BP; 7 A; 11 C; 6 G; 12 T; 0 other;

Query Match 63.0%; Score 12.6; DB 21; Length 36;
Best Local Similarity 78.9%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ttctgcgtctgagcattgc 19
||||||||| || || |
Db 14 ttctgcgtctaaggcttac 32

RESULT 14
AAZ59653
ID AAZ59653 standard; DNA; 36 BP.
XX
AC AAZ59653;
XX
DT 19-APR-2000 (first entry)
XX
DE Phytase-1 K91A mutagenic primer #1.
XX
KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
KW thermostable; animal feed; monogastric animal; phytate phosphorus;
KW phosphate availibility; consensus; phytase-1; mutagenesis; PCR primer;
KW ss.
XX
OS Aspergillus terreus 9A1.
OS Aspergillus terreus cbs16.46.
OS Aspergillus niger var. awamori.
OS Aspergillus niger T213.
OS Aspergillus niger str. NRRL3135.
OS Aspergillus fumigatus ATCC13073.
OS Aspergillus fumigatus ATCC32722.
OS Aspergillus fumigatus ATCC58128.
OS Aspergillus fumigatus ATCC26906.
OS Aspergillus fumigatus ATCC32239.
OS Emericella nidulans.
OS Talaromyces thermophilus ATCC20186.
OS Myceliophthora thermophila.
OS Synthetic.
XX
PN EP969089-A1.
XX
PD 05-JAN-2000.
XX
PF 23-JUN-1999; 99EP-0111949.
XX
PR 29-JUN-1998; 98EP-0111960.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Brugger R, Lehmann M, Wyss M;
XX
DR WPI; 2000-099429/09.
XX
PT New stabilized enzyme formulation, useful for feed compositions for
PT monogastric animals -
XX
PS Example 5; Page 19; 101pp; English.
XX
CC The invention relates to a novel stabilised dry or liquid enzyme
CC formulation, comprising phytase (myo-inositol hexakisphosphate
CC phosphohydrolase) and one or more stabilising agents including
CC xylitol or ribitol; polyethylene glycols with a molecular weight of 600
CC to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
CC glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
CC The stabilised phytase formulation is used in a method for preparing a
CC feed composition for monogastric animals (e.g., pigs, poultry) and
CC provides a monogastric animal with its dietary requirements of
CC phosphorus. Although a large amount of phosphate is present in animal
CC feed in the form of phytate phosphorus, monogastric animals are unable
CC to utilise this form of phosphate, resulting in the addition of extra
CC phosphate to the feed of such animals. Phytase enhances the nutritional
CC value of plant material without the need for adding additional phosphate
CC to the feed. The level of phosphate pollution in the environment is
CC reduced by adding phytase to animal feed, as the animal can make use of
CC the inorganic phosphate liberated from phytate phosphorus using the
CC enzyme. The phytase formulation of the invention has an improved
CC thermostability and can therefore remain stable during long-term storage
CC and can withstand feed processing methods such as extrusion, expansion
CC and pelleting. Sequences AAZ59643-Z59714 represent mutagenic PCR
CC primers used to introduce mutations into DNA encoding the consensus
CC phytase-1 (AAY69558) in order to increase the thermostability of
CC phytase-1. The mutations introduced were based on amino acid sequence
CC differences between phytase-1 and phytases 10 and 11 (AAY69566-Y69567).
XX
SQ Sequence 36 BP; 7 A; 11 C; 6 G; 12 T; 0 other;

Query Match 63.0%; Score 12.6; DB 21; Length 36;
Best Local Similarity 78.9%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ttctgcgtctgagcattgc 19
||||||||| || || |
Db 14 ttctgcgtctaaggcttac 32

RESULT 15
AAZ59654/c
ID AAZ59654 standard; DNA; 36 BP.
XX
AC AAZ59654;
XX
DT 19-APR-2000 (first entry)
XX
DE Phytase-1 K91A mutagenic primer #2.
XX
KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
KW thermostable; animal feed; monogastric animal; phytate phosphorus;
KW phosphate availibility; consensus; phytase-1; mutagenesis; PCR primer;
KW ss.
XX
OS Aspergillus terreus 9A1.
OS Aspergillus terreus cbs16.46.
OS Aspergillus niger var. awamori.
OS Aspergillus niger T213.
OS Aspergillus niger str. NRRL3135.
OS Aspergillus fumigatus ATCC13073.
OS Aspergillus fumigatus ATCC32722.
OS Aspergillus fumigatus ATCC58128.
OS Aspergillus fumigatus ATCC26906.
OS Aspergillus fumigatus ATCC32239.
OS Emericella nidulans.
OS Talaromyces thermophilus ATCC20186.
OS Myceliophthora thermophila.
OS Synthetic.
XX
PN EP969089-A1.
XX
PD 05-JAN-2000.
XX
PF 23-JUN-1999; 99EP-0111949.
XX
PR 29-JUN-1998; 98EP-0111960.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Brugger R, Lehmann M, Wyss M;
XX
DR WPI; 2000-099429/09.
XX
PT New stabilized enzyme formulation, useful for feed compositions for
PT monogastric animals -
XX
PS Example 5; Page 19; 101pp; English.
XX
CC The invention relates to a novel stabilised dry or liquid enzyme
CC formulation, comprising phytase (myo-inositol hexakisphosphate
CC phosphohydrolase) and one or more stabilising agents including
CC xylitol or ribitol; polyethylene glycols with a molecular weight of 600
CC to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
CC glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
CC The stabilised phytase formulation is used in a method for preparing a
CC feed composition for monogastric animals (e.g., pigs, poultry) and
CC provides a monogastric animal with its dietary requirements of
CC phosphorus. Although a large amount of phosphate is present in animal
CC feed in the form of phytate phosphorus, monogastric animals are unable
CC to utilise this form of phosphate, resulting in the addition of extra
CC phosphate to the feed of such animals. Phytase enhances the nutritional
CC value of plant material without the need for adding additional phosphate
CC to the feed. The level of phosphate pollution in the environment is
CC reduced by adding phytase to animal feed, as the animal can make use of
CC the inorganic phosphate liberated from phytate phosphorus using the
CC enzyme. The phytase formulation of the invention has an improved
CC thermostability and can therefore remain stable during long-term storage
CC and can withstand feed processing methods such as extrusion, expansion
CC and pelleting. Sequences AAZ59643-Z59714 represent mutagenic PCR
CC primers used to introduce mutations into DNA encoding the consensus
CC phytase-1 (AAY69558) in order to increase the thermostability of
CC phytase-1. The mutations introduced were based on amino acid sequence
CC differences between phytase-1 and phytases 10 and 11 (AAY69566-Y69567).
XX
SQ Sequence 36 BP; 12 A; 6 C; 11 G; 7 T; 0 other;

Query Match 63.0%; Score 12.6; DB 21; Length 36;
Best Local Similarity 78.9%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ttctgcgtctgagcattgc 19
|||||||||| || || |
Db 23 TTCTGCGTCTAAGGCTTAC 5

Search completed: March 13, 2002, 09:50:32
Job time: 5141 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 09:29:03 ; Search time 3124.31 Seconds
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Title: US-09-923-515-8
Perfect score: 20
Sequence: 1 tctgcgtctgagcattgcgt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
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14: gb_vi:*
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36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.		Score	Query Match	Length	DB	ID	Description
c	1	15	75.0	15	6	I35043	I35043 Sequence 11
c	2	13.2	66.0	28	6	A83871	A83871 Sequence 6
	3	12.8	64.0	21	12	AB068595	AB068595 Synthetic
c	4	12.6	63.0	25	6	E12345	E12345 Primer. 6/1
c	5	12.6	63.0	25	6	I21451	I21451 Sequence 12
c	6	12.6	63.0	51	6	AX157429	AX157429 Sequence
c	7	12.6	63.0	51	6	AX157430	AX157430 Sequence
	8	12.6	63.0	51	6	AX157994	AX157994 Sequence
c	9	12.6	63.0	51	6	AX160028	AX160028 Sequence
	10	12.4	62.0	20	6	AR031058	AR031058 Sequence
	11	12.4	62.0	20	6	AR043298	AR043298 Sequence
	12	12.4	62.0	20	6	AR074953	AR074953 Sequence
	13	12.4	62.0	20	6	I82149	I82149 Sequence 86
c	14	12.4	62.0	46	6	I36890	I36890 Sequence 10
c	15	12.4	62.0	46	6	I36891	I36891 Sequence 11
	16	12.4	62.0	46	6	I36892	I36892 Sequence 12
c	17	12.4	62.0	46	6	I48942	I48942 Sequence 4
c	18	12.4	62.0	46	6	I48943	I48943 Sequence 5
	19	12.4	62.0	46	6	I48944	I48944 Sequence 6
	20	12.4	62.0	60	6	AR043215	AR043215 Sequence
	21	12.4	62.0	60	6	AR074870	AR074870 Sequence
	22	12.4	62.0	60	6	I82066	I82066 Sequence 3
c	23	12.2	61.0	17	6	E00666	E00666 Oligonucleo
c	24	12.2	61.0	17	6	E00675	E00675 Oligonucleo
c	25	12.2	61.0	17	6	E00681	E00681 Oligonucleo
	26	12.2	61.0	20	12	AB069376	AB069376 Synthetic
c	27	12.2	61.0	37	6	I43879	I43879 Sequence 14
c	28	12	60.0	19	6	AR089051	AR089051 Sequence
c	29	12	60.0	19	6	AR140687	AR140687 Sequence
c	30	12	60.0	22	6	I77122	I77122 Sequence 8
c	31	12	60.0	25	6	I43029	I43029 Sequence 12
c	32	12	60.0	30	6	A21628	A21628 oligonucleo
c	33	12	60.0	30	6	I75993	I75993 Sequence 3
c	34	12	60.0	42	6	E31776	E31776 Hexurose ph
c	35	12	60.0	50	6	AR032644	AR032644 Sequence
c	36	12	60.0	50	6	AR032654	AR032654 Sequence
c	37	12	60.0	50	6	I29384	I29384 Sequence 25
c	38	12	60.0	50	6	I29394	I29394 Sequence 26
c	39	12	60.0	50	6	I43028	I43028 Sequence 11
c	40	12	60.0	50	6	I91058	I91058 Sequence 25
c	41	12	60.0	50	6	I91068	I91068 Sequence 26
	42	12	60.0	51	6	AX158420	AX158420 Sequence
c	43	12	60.0	56	6	AR082310	AR082310 Sequence
c	44	12	60.0	56	6	AR082327	AR082327 Sequence
c	45	12	60.0	56	6	AR120852	AR120852 Sequence

ALIGNMENTS

RESULT 1
I35043/c
LOCUS I35043 15 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 11 from patent US 5599706.
ACCESSION I35043
VERSION I35043.1 GI:2088011
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
TITLE Ribozymes targeted to apo(a) mRNA
JOURNAL Patent: US 5599706-A 11 04-FEB-1997;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
BASE COUNT 5 a 5 c 3 g 2 t
ORIGIN

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  Query Match             75.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 tgcgtctgagcattg 17
          ||||||||||||||||
Db     15 TGCGTCTGAGCATTG 1


RESULT   2
A83871/c
LOCUS       A83871         28 bp    DNA             PAT       21-JAN-2000
DEFINITION  Sequence 6 from Patent WO9848018.
ACCESSION   A83871
VERSION     A83871.1  GI:6733041
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Schneider-Fresenius,C. and Otto,B.
  TITLE     RECOMBINANT HUMAN BETA INTERFERON WITH ENHANCED SOLUBILITY
  JOURNAL   Patent: WO 9848018-A 6 29-OCT-1998;
            SCHNEIDER FRESENIUS CHRISTIAN (DE); OTTO BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        8 a      10 c       5 g       5 t
ORIGIN


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  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 tctgcgtctgagcattgc 18
          |||| | |||||  |||||
Db     22 TCTGGGACTGAGAATTGC 5


RESULT   3
AB068595
LOCUS       AB068595       21 bp    DNA             SYN       08-AUG-2001
DEFINITION  Synthetic construct DNA, reverse primer for human STS sts-stSG27932
            at 1p36.
ACCESSION   AB068595
VERSION     AB068595.1  GI:15129399
KEYWORDS    .
SOURCE      synthetic construct DNA.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A bac-based sts-content map spanning a 35-mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics. 74 (1), 55-70 (2001)
  MEDLINE   21269192
REFERENCE   2  (bases 1 to 21)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
     misc_feature    1. .21
                     /note="reverse primer for human STS sts-stSG27932 at 1p36
                     sts-stSG27932 obtained from clones B72G3, B370L16,
                     B341F17, B265D10, B341F17, B53F6, B128O2, B85K5, B73C3,
                     Human BAC library RPCI-11"
BASE COUNT        2 a       7 c       4 g       8 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 12;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 3.4e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tctgcgtctgagcatt 16
          ||| ||||||| ||||
Db      2 TCTCCGTCTGACCATT 17


RESULT   4
E12345/c
LOCUS       E12345         25 bp    DNA             PAT       24-JUN-1998
DEFINITION  Primer.
ACCESSION   E12345
VERSION     E12345.1  GI:3251179
KEYWORDS    JP 1996308600-A/12.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Chiyunnshiyun,U., Chiyuufuan,R., Gannshiyun,K., Chiyannchien,F. and
            Chinnmin,C. .
  TITLE     OLIGONUCLEOTIDE FOR BACULOVIRUS INFECTION DETECTION
  JOURNAL   Patent: JP 1996308600-A 12 26-NOV-1996;
            NATL SCI KAUNSHIRU
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996308600-A/12
            PD   26-NOV-1996
            PF   05-JAN-1995 JP 1995016515
            PI   CHIYUNNSHIYUN UAN, CHIYUUFUAN RO, GANNSHIYUN KOU, PI
            CHIYANNCHIEN FUAN,
            PI   CHINNMIN CHIYOU
            PC   C12Q1/70,C07H21/04,C12N15/09,C12Q1/68;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .25
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        6 a       6 c       5 g       8 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 25;
  Best Local Similarity   78.9%;  Pred. No. 4.3e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 ctgcgtctgagcattgcgt 20
          | |||||| ||  |||||||
Db     24 CGGCGTCTAAGATTTGCGT 6


RESULT   5
I21451/c
LOCUS       I21451         25 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 12 from patent US 5521299.
ACCESSION   I21451
VERSION     I21451.1  GI:1601805
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Wang,C., Lo,C., Kou,G., Huang,C. and Chou,C.
  TITLE     Oligonucleotides for detection of baculovirus infection
  JOURNAL   Patent: US 5521299-A 12 28-MAY-1996;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
BASE COUNT        6 a      6 c      5 g      8 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 25;
  Best Local Similarity   78.9%;  Pred. No. 4.3e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 ctgcgtctgagcattgcgt 20
          | |||||| ||  ||||||
Db     24 CGGCGTCTAAGATTTGCGT 6


RESULT   6
AX157429/c
LOCUS       AX157429       51 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 757 from Patent WO0140521.
ACCESSION   AX157429
VERSION     AX157429.1  GI:14538760
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 757 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="1 of 2 allelic variants (758 is other entry)
                     Accession number cg21428762"
BASE COUNT       15 a     11 c     19 g      6 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 51;
  Best Local Similarity   78.9%;  Pred. No. 4.2e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 tctgcgtctgagcattgcg 19
          |||||||| |||||   ||
Db     41 TCTGCGTCCGAGCACCCCG 23


RESULT   7
AX157430/c
LOCUS       AX157430       51 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 758 from Patent WO0140521.
ACCESSION   AX157430
VERSION     AX157430.1  GI:14538761
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 758 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="2 of 2 allelic variants (757 is other entry)
                     Accession number cg21428762"
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  Best Local Similarity   78.9%;  Pred. No. 4.2e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 tctgcgtctgagcattgcg 19
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Db     41 TCTGCGTCCGAGCACACCG 23


RESULT   8
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LOCUS       AX157994       51 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 1322 from Patent WO0140521.
ACCESSION   AX157994
VERSION     AX157994.1  GI:14539325
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 1322 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
     misc_feature    26
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                     Accession number cg28972181"
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ORIGIN


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  Best Local Similarity   78.9%;  Pred. No. 4.2e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 ctgcgtctgagcattgcgt 20
          | ||||| | ||||| |||
Db     16 CAGCGTCGGGGCATTACGT 34


RESULT   9
AX160028/c
LOCUS       AX160028       51 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 3356 from Patent WO0140521.
ACCESSION   AX160028
VERSION     AX160028.1  GI:14541359
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 3356 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN


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  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 ctgcgtctgagcattgcgt 20
          ||| ||||| ||||| | |
Db     39 CTGTGTCTGTGCATTCCAT 21


RESULT  10
AR031058
LOCUS       AR031058       20 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 46 from patent US 5861504.
ACCESSION   AR031058
VERSION     AR031058.1  GI:5944272
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Polymeropoulos,M.H. and Merril,C.R.
  TITLE     Eleven highly informative microsatelite repeat polymorphic DNA
            markers
  JOURNAL   Patent: US 5861504-A 46 19-JAN-1999;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT        5 a      4 c      6 g      5 t
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  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ctgcgtctgagcat 15
          |||| |||||||||
Db      1 CTGCATCTGAGCAT 14


RESULT  11
AR043298
LOCUS       AR043298       20 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 86 from patent US 5814457.
ACCESSION   AR043298
VERSION     AR043298.1  GI:5964306
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kern,S.E. and Hahn,S.A.
  TITLE     DPC4 polypeptide
  JOURNAL   Patent: US 5814457-A 86 29-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      3 c      6 g      7 t
ORIGIN


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  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      6 gtctgagcattgcg 19
          |||||||||||| |
Db      2 GTCTGAGCATTGTG 15


RESULT  12
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LOCUS       AR074953       20 bp    DNA             PAT       28-AUG-2000
DEFINITION  Sequence 86 from patent US 5955292.
ACCESSION   AR074953
VERSION     AR074953.1  GI:10001705
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kern,S.E. and Hahn,S.A.
  TITLE     Tumor suppressor gene, DPC4
  JOURNAL   Patent: US 5955292-A 86 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      3 c      6 g      7 t
ORIGIN


  Query Match            62.0%;  Score 12.4;  DB 6;  Length 20;
  Best Local Similarity  92.9%;  Pred. No. 5.6e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      6 gtctgagcattgcg 19
          |||||||||||| |
Db      2 GTCTGAGCATTGTG 15


RESULT  13
I82149
LOCUS       I82149         20 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 86 from patent US 5712097.
ACCESSION   I82149
VERSION     I82149.1  GI:3210446
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kern,S.E. and Hahn,S.A.
  TITLE     Tumor suppressor gene, DPC4
  JOURNAL   Patent: US 5712097-A 86 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        4 a      3 c      6 g      7 t
ORIGIN


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  Best Local Similarity  92.9%;  Pred. No. 5.6e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      6 gtctgagcattgcg 19
          |||||||||||| |
Db      2 GTCTGAGCATTGTG 15
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RESULT  14
I36890/c
LOCUS       I36890         46 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 10 from patent US 5612196.
ACCESSION   I36890
VERSION     I36890.1  GI:2084850
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Becquart,J.erome, Fleer,R. and Jung,G.erard.
  TITLE     Human serun albumin, preparation and use
  JOURNAL   Patent: US 5612196-A 10 18-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="unknown"
BASE COUNT       18 a     18 c      3 g      7 t
ORIGIN


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  Best Local Similarity   92.9%;  Pred. No. 5.5e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      7 tctgagcattgcgt 20
          ||||| ||||||||
Db     44 TCTGAACATTGCGT 31


RESULT  15
I36891/c
LOCUS       I36891         46 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 11 from patent US 5612196.
ACCESSION   I36891
VERSION     I36891.1  GI:2084851
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Becquart,J.erome, Fleer,R. and Jung,G.erard.
  TITLE     Human serun albumin, preparation and use
  JOURNAL   Patent: US 5612196-A 11 18-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="unknown"
BASE COUNT       16 a     18 c      5 g      7 t
ORIGIN


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  Best Local Similarity   92.9%;  Pred. No. 5.5e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      7 tctgagcattgcgt 20
          ||||| ||||||||
Db     44 TCTGAACATTGCGT 31


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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

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Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.		Score	Query Match	Length	DB	ID	Description
c	1	15	75.0	15	6	I35115	I35115 Sequence 83
c	2	14.4	72.0	42	6	A70339	A70339 Sequence 6
c	3	14.4	72.0	42	6	AR117156	AR117156 Sequence
	4	14.2	71.0	24	6	A30267	A30267 Nisin Z PCR
	5	14.2	71.0	24	6	I33938	I33938 Sequence 10
	6	13.8	69.0	29	6	AX077820	AX077820 Sequence
c	7	13.6	68.0	24	6	AX111647	AX111647 Sequence
c	8	13.6	68.0	29	6	AR049956	AR049956 Sequence
c	9	13.6	68.0	29	6	AR052306	AR052306 Sequence
c	10	13.6	68.0	29	6	AR076510	AR076510 Sequence
c	11	13.6	68.0	29	6	AR099642	AR099642 Sequence
c	12	13.6	68.0	29	6	I12959	I12959 Sequence 15
c	13	13.6	68.0	29	6	I32930	I32930 Sequence 2
c	14	13.6	68.0	29	6	I34536	I34536 Sequence 31
c	15	13.6	68.0	29	6	I39806	I39806 Sequence 31
c	16	13.6	68.0	29	6	I43646	I43646 Sequence 4
c	17	13.6	68.0	29	6	I90316	I90316 Sequence 2
c	18	13.6	68.0	48	6	AR049962	AR049962 Sequence
c	19	13.6	68.0	48	6	AR099648	AR099648 Sequence
c	20	13.6	68.0	48	6	I34542	I34542 Sequence 41
	21	13.2	66.0	29	6	I12960	I12960 Sequence 16
c	22	13.2	66.0	35	6	AX116034	AX116034 Sequence
c	23	13.2	66.0	37	6	I42715	I42715 Sequence 11
	24	13.2	66.0	51	6	AX160737	AX160737 Sequence
	25	13.2	66.0	51	6	AX160738	AX160738 Sequence
c	26	13	65.0	22	6	I79232	I79232 Sequence 5
	27	13	65.0	28	6	AR097020	AR097020 Sequence
	28	12.8	64.0	33	6	AR049551	AR049551 Sequence
	29	12.8	64.0	33	6	AR065756	AR065756 Sequence
c	30	12.8	64.0	36	6	AR068333	AR068333 Sequence
	31	12.8	64.0	56	6	AX003488	AX003488 Sequence
c	32	12.6	63.0	44	6	AR061552	AR061552 Sequence
c	33	12.6	63.0	44	6	AR108451	AR108451 Sequence
c	34	12.6	63.0	44	6	I16408	I16408 Sequence 23
c	35	12.6	63.0	44	6	I66894	I66894 Sequence 23
c	36	12.6	63.0	44	6	I84988	I84988 Sequence 23
	37	12.6	63.0	51	6	AX160379	AX160379 Sequence
	38	12.6	63.0	51	6	AX160380	AX160380 Sequence
	39	12.6	63.0	51	6	AX160381	AX160381 Sequence
	40	12.4	62.0	19	6	AX129550	AX129550 Sequence
	41	12.4	62.0	19	6	AX129551	AX129551 Sequence
	42	12.4	62.0	19	6	AX129552	AX129552 Sequence
	43	12.4	62.0	44	6	AR075944	AR075944 Sequence
	44	12.2	61.0	30	6	I24980	I24980 Sequence 13
	45	12.2	61.0	30	6	I92699	I92699 Sequence 13

ALIGNMENTS

RESULT 1
I35115/c
LOCUS I35115 15 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 83 from patent US 5599706.
ACCESSION I35115
VERSION I35115.1 GI:2088083
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
TITLE Ribozymes targeted to apo(a) mRNA
JOURNAL Patent: US 5599706-A 83 04-FEB-1997;
FEATURES Location/Qualifiers
source 1. .15
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BASE COUNT 3 a 1 c 3 g 8 t
ORIGIN

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 aaaagcttatacaca 20
          ||||||||||||||||
Db     15 AAAAGCTTATACACA 1


RESULT   2
A70339/c
LOCUS       A70339         42 bp    DNA             PAT       07-MAY-1999
DEFINITION  Sequence 6 from Patent WO9810080.
ACCESSION   A70339
VERSION     A70339.1  GI:4774632
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Ledeboer,A.M., Kok,J., Venema,G. and Sanders,J.W.
  TITLE     SALT-INDUCIBLE PROMOTER DERIVABLE FROM A LACTIC ACID BACTERIUM, AND
            ITS USE IN A LACTIC ACID BACTERIUM FOR PRODUCTION OF A DESIRED
            PROTEIN
  JOURNAL   Patent: WO 9810080-A 6 12-MAR-1998;
            UNILEVER PLC (GB)
FEATURES             Location/Qualifiers
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  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 cttaaaagcttataca 18
          | ||||||||||||||
Db     36 CATAAAAGCTTATACA 21


RESULT   3
AR117156/c
LOCUS       AR117156       42 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 6 from patent US 6140078.
ACCESSION   AR117156
VERSION     AR117156.1  GI:14098062
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Sanders,J.W., Kok,J., Venema,G. and Ledeboer,A.M.
  TITLE     Salt-inducible promoter derivable from a lactic acid bacterium, and
            its use in a lactic acid bacterium for production of a desired
            protein
  JOURNAL   Patent: US 6140078-A 6 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .42
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BASE COUNT        8 a      8 c     10 g     16 t
ORIGIN


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  Best Local Similarity   93.8%;  Pred. No. 1.6e+04;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 cttaaaagcttataca 18
          | ||||||||||||||
Db     36 CATAAAAGCTTATACA 21


RESULT   4
A30267
LOCUS       A30267         24 bp    DNA             PAT       03-OCT-1995
DEFINITION  Nisin Z PCR mutagenic primer HindIII (flanking primer).
ACCESSION   A30267
VERSION     A30267.1  GI:1249097
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   .
  TITLE     LANTIBIOTICS SIMILAR TO NISIN A, LACTIC ACID BACTERIA WHICH PRODUCE
            SUCH LANTIBIOTICS, METHOD FOR CONSTRUCTING SUCH LACTIC ACID
            BACTERIA AND METHOD FOR PRESERVING FOODSTUFFS WITH THE AID OF THESE
            LANTIBIOTICS AND THESE LACTIC ACID BACTERIA PRODUCING LANTIBIOTICS
  JOURNAL   Patent: WO 9218633-A 2 29-OCT-1992;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
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BASE COUNT       12 a      4 c      3 g      5 t
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  Best Local Similarity   84.2%;  Pred. No. 2.2e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 ccttaaaagcttatacaca 20
          ||| |||||||||| | |
Db      2 CCTAAAAAGCTTATAAAAA 20


RESULT   5
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LOCUS       I33938         24 bp    DNA             PAT       06-FEB-1997
DEFINITION  Sequence 10 from patent US 5594103.
ACCESSION   I33938
VERSION     I33938.1  GI:1824729
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   De Vos,W.M., Siezen,R.J. and Kuipers,O.P.
  TITLE     Lantibiotics similar to nisin a
  JOURNAL   Patent: US 5594103-A 10 14-JAN-1997;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
BASE COUNT       12 a      4 c      3 g      5 t
ORIGIN


  Query Match             71.0%;  Score 14.2;  DB 6;  Length 24;
  Best Local Similarity   84.2%;  Pred. No. 2.2e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 ccttaaaagcttatacaca 20
          ||| |||||||||| | |
Db      2 CCTAAAAAGCTTATAAAAA 20


RESULT   6
AX077820
LOCUS       AX077820       29 bp    DNA             PAT       22-FEB-2001
DEFINITION  Sequence 21 from Patent WO0107627.
ACCESSION   AX077820
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VERSION     AX077820.1  GI:13157676
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Eisen,A.
  TITLE     Drosophila recombination-associated protein and methods for use
  JOURNAL   Patent: WO 0107627-A 21 01-FEB-2001;
            ALBERT EINSTEIN COLLEGE OF MEDICINE OF YESHIVA UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
BASE COUNT        9 a      8 c      4 g      8 t
ORIGIN


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  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 ccttaaaagcttataca 18
          ||| |||||||||| ||
Db      4 CCTGAAAAGCTTATTCA 20


RESULT   7
AX111647/c
LOCUS       AX111647       24 bp    DNA             PAT       30-APR-2001
DEFINITION  Sequence 22 from Patent WO0125419.
ACCESSION   AX111647
VERSION     AX111647.1  GI:13927923
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Conrad,C.A. and Chen,Y.
  TITLE     Altering gene expression with ssdna produced in vivo
  JOURNAL   Patent: WO 0125419-A 22 12-APR-2001;
            Cytogenix, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
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                     /note="Synthetic oligonucleotide"
BASE COUNT        4 a      6 c      6 g      8 t
ORIGIN


  Query Match            68.0%;  Score 13.6;  DB 6;  Length 24;
  Best Local Similarity  80.0%;  Pred. No. 4.1e+04;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 accttaaaagcttatacaca 20
          ||||  ||||||| | ||||
Db     22 ACCTGCAAAGCTTGTGCACA 3


RESULT   8
AR049956/c
LOCUS       AR049956       29 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 31 from patent US 5824792.
ACCESSION   AR049956
VERSION     AR049956.1  GI:5971948
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Payne,J.M., Kennedy,M.Keith, Randall,J.Brookes, Meier,H.,
            Uick,H.Jane, Foncerrada,L., Schnepf,H.Ernest, Schwab,G.E. and Fu,J.
  TITLE     Bacillus thuringiensis toxins active against hymenopteran pests
  JOURNAL   Patent: US 5824792-A 31 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
BASE COUNT        6 a      3 c      4 g      12 t      4 others
ORIGIN


  Query Match            68.0%;  Score 13.6;  DB 6;  Length 29;
  Best Local Similarity  81.2%;  Pred. No. 4e+04;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 ttaaaagcttatacac 19
          ||||||:| :||||||
Db     20 TTAAAASCGWATACAC 5


RESULT   9
AR052306/c
LOCUS       AR052306       29 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 2 from patent US 5831011.
ACCESSION   AR052306
VERSION     AR052306.1  GI:5975670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Payne,J., Narva,K.E. and Fu,J.
  TITLE     Bacillus thuringiensis genes encoding nematode-active toxins
  JOURNAL   Patent: US 5831011-A 2 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
BASE COUNT        6 a      3 c      4 g      12 t      4 others
ORIGIN


  Query Match            68.0%;  Score 13.6;  DB 6;  Length 29;
  Best Local Similarity  81.2%;  Pred. No. 4e+04;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 ttaaaagcttatacac 19
          ||||||:| :||||||
Db     20 TTAAAASCGWATACAC 5


RESULT  10
AR076510/c
LOCUS       AR076510       29 bp    DNA             PAT       30-AUG-2000
DEFINITION  Sequence 2 from patent US 5959080.
ACCESSION   AR076510
VERSION     AR076510.1  GI:10003256
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Payne,J., Narva,K.E. and Fu,J.
  TITLE     Bacillus thuringiensis genes encoding nematode-active toxins
  JOURNAL   Patent: US 5959080-A 2 28-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
BASE COUNT        6 a      3 c      4 g      12 t      4 others
ORIGIN


  Query Match            68.0%;  Score 13.6;  DB 6;  Length 29;
  Best Local Similarity  81.2%;  Pred. No. 4e+04;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy      4 ttaaaagcttatacac 19
          |||||||:| :|||||||
Db     20 TTAAAASCGWATACAC 5


RESULT  11
AR099642/c
LOCUS       AR099642        29 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 31 from patent US 6077937.
ACCESSION   AR099642
VERSION     AR099642.1  GI:12809408
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Payne,J.M., Kennedy,M.Keith, Randall,J.Brookes, Meier,H.,
            Uick,H.Jane, Foncerrada,L., Schnepf,H.Ernest, Schwab,G.E. and Fu,J.
  TITLE     Bacillus thuringiensis toxins active against hymenopteran pests
  JOURNAL   Patent: US 6077937-A 31 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
BASE COUNT        6 a      3 c      4 g     12 t      4 others
ORIGIN


  Query Match             68.0%;  Score 13.6;  DB 6;  Length 29;
  Best Local Similarity   81.2%;  Pred. No. 4e+04;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 ttaaaagcttatacac 19
          |||||||:| :|||||||
Db     20 TTAAAASCGWATACAC 5


RESULT  12
I12959/c
LOCUS       I12959          29 bp    DNA             PAT       26-JUL-1995
DEFINITION  Sequence 15 from patent US 5430137.
ACCESSION   I12959
VERSION     I12959.1  GI:910936
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Gaertner,F.H., Sick,A.J., Thompson,M., Schnepf,H.Ernest,
            Schwab,G.E. and Narva,K.E.
  TITLE     Probes for the identification of Bacillus thuringiensis endotoxin
            genes
  JOURNAL   Patent: US 5430137-A 15 04-JUL-1995;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
BASE COUNT        6 a      3 c      4 g     12 t      4 others
ORIGIN


  Query Match             68.0%;  Score 13.6;  DB 6;  Length 29;
  Best Local Similarity   81.2%;  Pred. No. 4e+04;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 ttaaaagcttatacac 19
          |||||||:| :|||||||
Db     20 TTAAAASCGWATACAC 5


RESULT  13
I32930/c
LOCUS       I32930          29 bp    DNA             PAT       06-FEB-1997
DEFINITION  Sequence 2 from patent US 5589382.
ACCESSION   I32930
VERSION     I32930.1  GI:1823721
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Payne,J., Narva,K.E. and Fu,J.
  TITLE     Bacillus thuringiensis genes encoding nematode-active toxins
  JOURNAL   Patent: US 5589382-A 2 31-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
BASE COUNT        6 a      3 c      4 g     12 t      4 others
ORIGIN


  Query Match             68.0%;  Score 13.6;  DB 6;  Length 29;
  Best Local Similarity   81.2%;  Pred. No. 4e+04;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 ttaaaagcttatacac 19
          |||||||:| :|||||||
Db     20 TTAAAASCGWATACAC 5


RESULT  14
I34536/c
LOCUS       I34536          29 bp    DNA             PAT       06-FEB-1997
DEFINITION  Sequence 31 from patent US 5596071.
ACCESSION   I34536
VERSION     I34536.1  GI:1825327
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Payne,J.M., Kennedy,M.Keith, Randall,J.B., Meier,H., Uick,H.J.,
            Foncerrada,L., Schnepf,H.Ernest, Schwab,G.E. and Fu,J.
  TITLE     Bacillus thuringiensis toxins active against hymenopteran pests
  JOURNAL   Patent: US 5596071-A 31 21-JAN-1997;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
BASE COUNT        6 a      3 c      4 g     12 t      4 others
ORIGIN


  Query Match             68.0%;  Score 13.6;  DB 6;  Length 29;
  Best Local Similarity   81.2%;  Pred. No. 4e+04;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 ttaaaagcttatacac 19
          |||||||:| :|||||||
Db     20 TTAAAASCGWATACAC 5


RESULT  15
I39806/c
LOCUS       I39806          29 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 31 from patent US 5616495.
ACCESSION   I39806
VERSION     I39806.1  GI:2084286
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Payne,J.M., Kennedy,M.Keith, Randall,J.B., Meier,H., Uick,H.J.,
            Foncerrada,L., Schnepf,H.E. and Schwab,G.E.
  TITLE     Bacillus thuringiensis gene encoding hymenopteran-active toxins
  JOURNAL   Patent: US 5616495-A 31 01-APR-1997;
FEATURES             Location/Qualifiers
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     source          1. .29
                     /organism="unknown"
BASE COUNT        6 a      3 c      4 g     12 t      4 others
ORIGIN


  Query Match             68.0%;  Score 13.6;  DB 6;  Length 29;
  Best Local Similarity   81.2%;  Pred. No. 4e+04;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       4 ttaaaagcttatacac 19
           ||||||:| :||||||
Db      20 TTAAAASCGWATACAC 5


Search completed: March 13, 2002, 10:38:55
Job time: 4152 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 10:38:43 ; Search time 2671.52 Seconds
(without alignments)
123.504 Million cell updates/sec

Title: US-09-923-515-29
Perfect score: 20
Sequence: 1 acaccaagggcgaatctcag 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
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27: em_sy:*
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30: em_htgo_hum:*
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32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	15	75.0	15	6	I35069	I35069 Sequence 37
c 2	15	75.0	15	6	I35070	I35070 Sequence 38
3	14.2	71.0	53	6	I26223	I26223 Sequence 8
4	14.2	71.0	54	6	A25801	A25801 motif for a
5	14.2	71.0	54	6	A26046	A26046 CEB5 from c
c 6	13.8	69.0	22	6	AX110597	AX110597 Sequence
7	13.8	69.0	57	6	I14478	I14478 Sequence 2
8	13.4	67.0	36	6	A18355	A18355 Oligonucleo
c 9	13.4	67.0	37	6	A18356	A18356 Oligonucleo
10	13.2	66.0	50	6	AX162336	AX162336 Sequence
11	13.2	66.0	50	6	AX162338	AX162338 Sequence
c 12	13	65.0	15	6	I35071	I35071 Sequence 39
c 13	13	65.0	15	6	I35235	I35235 Sequence 20
14	12.8	64.0	32	6	AX003160	AX003160 Sequence
15	12.8	64.0	32	6	AX018574	AX018574 Sequence
16	12.8	64.0	32	6	AX018650	AX018650 Sequence
17	12.8	64.0	32	6	AX023703	AX023703 Sequence
18	12.8	64.0	51	6	AX162335	AX162335 Sequence
19	12.8	64.0	51	6	AX162337	AX162337 Sequence
20	12.6	63.0	33	6	AX168028	AX168028 Sequence
21	12.6	63.0	39	6	AX057115	AX057115 Sequence
22	12.6	63.0	50	6	AX063400	AX063400 Sequence
c 23	12.6	63.0	51	6	AX165209	AX165209 Sequence
24	12.2	61.0	19	6	I14335	I14335 Sequence 5
25	12.2	61.0	41	6	AX135990	AX135990 Sequence
26	12.2	61.0	41	6	AX136047	AX136047 Sequence
c 27	12	60.0	40	6	AR039004	AR039004 Sequence
c 28	12	60.0	40	6	AR039006	AR039006 Sequence
c 29	12	60.0	40	6	AR107396	AR107396 Sequence
c 30	12	60.0	40	6	AR107398	AR107398 Sequence
31	12	60.0	50	6	AR036494	AR036494 Sequence
32	12	60.0	50	6	AR081021	AR081021 Sequence
c 33	11.8	59.0	17	6	AR006808	AR006808 Sequence
c 34	11.8	59.0	17	6	AR008988	AR008988 Sequence
c 35	11.8	59.0	17	6	AR135416	AR135416 Sequence
c 36	11.8	59.0	17	6	I61187	I61187 Sequence 12
c 37	11.8	59.0	17	6	I71320	I71320 Sequence 58
c 38	11.8	59.0	17	6	I78736	I78736 Sequence 12
39	11.8	59.0	21	6	AX092710	AX092710 Sequence
c 40	11.8	59.0	21	6	E14786	E14786 PCR primer.
c 41	11.8	59.0	23	22	E09106	E09106 Synthetic o
c 42	11.8	59.0	24	6	AR075264	AR075264 Sequence
c 43	11.8	59.0	24	6	AR129602	AR129602 Sequence
c 44	11.8	59.0	24	6	AR152676	AR152676 Sequence
c 45	11.8	59.0	24	6	I61288	I61288 Sequence 95

ALIGNMENTS

RESULT 1
I35069/c
LOCUS I35069 15 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 37 from patent US 5599706.
ACCESSION I35069
VERSION I35069.1 GI:2088037
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
TITLE Ribozymes targeted to apo(a) mRNA
JOURNAL Patent: US 5599706-A 37 04-FEB-1997;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
BASE COUNT 2 a 5 c 3 g 5 t
ORIGIN

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  Query Match             75.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 aagggcgaatctcag 20
          |||||||||||||||
Db     15 AAGGGCGAATCTCAG 1


RESULT   2
I35070/c
LOCUS       I35070         15 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 38 from patent US 5599706.
ACCESSION   I35070
VERSION     I35070.1  GI:2088038
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 38 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        2 a      4 c      4 g      5 t
ORIGIN


  Query Match             75.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 caagggcgaatctca 19
          |||||||||||||||
Db     15 CAAGGGCGAATCTCA 1


RESULT   3
I26223
LOCUS       I26223         53 bp    DNA             PAT       07-OCT-1996
DEFINITION  Sequence 8 from patent US 5556955.
ACCESSION   I26223
VERSION     I26223.1  GI:1606093
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Vergnaud,G.
  TITLE     Process for detection of new polymorphic loci in a DNA sequence,
            nucleotide sequences forming hybridization probes and their
            applications
  JOURNAL   Patent: US 5556955-A 8 17-SEP-1996;
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="unknown"
BASE COUNT        8 a      22 c     12 g     11 t
ORIGIN


  Query Match             71.0%;  Score 14.2;  DB 6;  Length 53;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 caccaagggcgaatctcag 20
          |||| ||| ||||||||  |
Db      9 CACCCAGGTCGAATCTCGG 27


RESULT   4
```

```
A25801
LOCUS       A25801         54 bp    DNA             PAT       14-MAR-1995
DEFINITION  motif for a 7th sequence (with form.3).
ACCESSION   A25801
VERSION     A25801.1  GI:904769
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   .
  JOURNAL   Patent: FR 2680520-A 8 26-FEB-1993;
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        8 a      22 c     13 g     11 t
ORIGIN


  Query Match             71.0%;  Score 14.2;  DB 6;  Length 54;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 caccaagggcgaatctcag 20
          |||| ||| ||||||||  |
Db      9 CACCCAGGTCGAATCTCGG 27


RESULT   5
A26046
LOCUS       A26046         54 bp    DNA             PAT       14-MAR-1995
DEFINITION  CEB5 from cosmide 61.
ACCESSION   A26046
VERSION     A26046.1  GI:904818
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   .
  JOURNAL   Patent: FR 2680520-A 41 26-FEB-1993;
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        8 a      22 c     13 g     11 t
ORIGIN


  Query Match             71.0%;  Score 14.2;  DB 6;  Length 54;
  Best Local Similarity   84.2%;  Pred. No. 2.1e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 caccaagggcgaatctcag 20
          |||| ||| ||||||||  |
Db      9 CACCCAGGTCGAATCTCGG 27


RESULT   6
AX110597/c
LOCUS       AX110597       22 bp    DNA             PAT       30-APR-2001
DEFINITION  Sequence 1330 from Patent WO0123604.
ACCESSION   AX110597
VERSION     AX110597.1  GI:13926889
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
```

```
          for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1330 05-APR-2001;
          Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
BASE COUNT        4 a      3 c      9 g      6 t
ORIGIN
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  Query Match             69.0%;  Score 13.8;  DB 6;  Length 22;
  Best Local Similarity   88.2%;  Pred. No. 4.1e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 acaccaagggcgaatct 17
          ||||||||  |||||||
Db     17 ACACCAAGTTCGAATCT 1
```

```
RESULT   7
I14478
LOCUS       I14478         57 bp    DNA             PAT       26-SEP-1995
DEFINITION  Sequence 2 from patent US 5451499.
ACCESSION   I14478
VERSION     I14478.1  GI:996961
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 57)
  AUTHORS   Cochran,M.D.
  TITLE     Attenuated, genetically-engineered pseudorabies virus S-PRV-155 and
            uses thereof
  JOURNAL   Patent: US 5451499-A 2 19-SEP-1995;
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="unknown"
BASE COUNT       10 a     17 c     23 g      7 t
ORIGIN
```

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  Query Match             69.0%;  Score 13.8;  DB 6;  Length 57;
  Best Local Similarity   88.2%;  Pred. No. 3.4e+04;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 acaccaagggcgaatct 17
          |||||||| ||| |||
Db     17 ACACCAAGGTCGACTCT 33
```

```
RESULT   8
A18355
LOCUS       A18355         36 bp    DNA             PAT       26-APR-1994
DEFINITION  Oligonucleotide 3 for production of the BglI/EcoRI gene segment.
ACCESSION   A18355
VERSION     A18355.1  GI:513268
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   .
  TITLE     MULTIVALENT ANTIGEN-BINDING PROTEINS
  JOURNAL   Patent: WO 9119739-A 9 26-DEC-1991;
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        9 a     12 c      8 g      7 t
ORIGIN
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  Query Match             67.0%;  Score 13.4;  DB 6;  Length 36;
  Best Local Similarity   93.3%;  Pred. No. 5.9e+04;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 caccaagggcgaatc 16
          ||||||||||| ||
Db     10 CACCAAGGGCGAGTC 24
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RESULT   9
A18356/c
LOCUS       A18356         37 bp    DNA             PAT       26-APR-1994
DEFINITION  Oligonucleotide 4 for production of the BglI/EcoRI gene segment.
ACCESSION   A18356
VERSION     A18356.1  GI:512257
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   .
  TITLE     MULTIVALENT ANTIGEN-BINDING PROTEINS
  JOURNAL   Patent: WO 9119739-A 10 26-DEC-1991;
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        7 a      8 c     13 g      9 t
ORIGIN
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```
  Query Match             67.0%;  Score 13.4;  DB 6;  Length 37;
  Best Local Similarity   93.3%;  Pred. No. 5.8e+04;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 caccaagggcgaatc 16
          ||||||||||| ||
Db     32 CACCAAGGGCGAGTC 18
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```
RESULT  10
AX162336
LOCUS       AX162336       50 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 5664 from Patent WO0140521.
ACCESSION   AX162336
VERSION     AX162336.1  GI:14543667
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 5664 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg44018633"
     misc_feature    26
                     /note="2 of 2 allelic variants (5663 is other entry)"
BASE COUNT       17 a     19 c     10 g      4 t
ORIGIN
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  Query Match             66.0%;  Score 13.2;  DB 6;  Length 50;
  Best Local Similarity   83.3%;  Pred. No. 6.9e+04;
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  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 caccaagggcgaatctca 19
          ||||||||| | |||| |
Db     10 CACCAAGGGAGCATCTGA 27


RESULT  11
AX162338
LOCUS       AX162338       50 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 5666 from Patent WO0140521.
ACCESSION   AX162338
VERSION     AX162338.1  GI:14543669
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 5666 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    25. .26
                     /note="Nucleotide deleted between bases 25 and 26
                     Accession number cg44018633"
     misc_feature    26
                     /note="2 of 2 allelic variants (5665 is other entry)"
BASE COUNT       17 a     18 c     10 g      5 t
ORIGIN


  Query Match             66.0%;  Score 13.2;  DB 6;  Length 50;
  Best Local Similarity   83.3%;  Pred. No. 6.9e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 caccaagggcgaatctca 19
          ||||||||| | |||| |
Db      9 CACCAAGGGAGCATCTGA 26


RESULT  12
I35071/c
LOCUS       I35071         15 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 39 from patent US 5599706.
ACCESSION   I35071
VERSION     I35071.1  GI:2088039
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 39 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        1 a      4 c      4 g      6 t
ORIGIN


  Query Match             65.0%;  Score 13;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 acaccaagggcga 13
          |||||||||||||
Db     13 ACACCAAGGGCGA 1


RESULT  13
I35235/c
LOCUS       I35235         15 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 203 from patent US 5599706.
ACCESSION   I35235
VERSION     I35235.1  GI:2088203
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 203 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        1 a      4 c      4 g      6 t
ORIGIN


  Query Match             65.0%;  Score 13;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 acaccaagggcga 13
          |||||||||||||
Db     13 ACACCAAGGGCGA 1


RESULT  14
AX003160
LOCUS       AX003160       32 bp    DNA             PAT       24-AUG-2000
DEFINITION  Sequence 11 from Patent WO9932646.
ACCESSION   AX003160
VERSION     AX003160.1  GI:9927022
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Carroll,M.W. and Mitrophanous,K.
  TITLE     Equine infectious anaemia virus (eiav) based
  JOURNAL   Patent: WO 9932646-A 11 01-JUL-1999;
            CARROLL MILES WILLIAM (GB); MITROPHANOUS KYRIACOS (GB)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT        8 a      9 c      8 g      7 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 6;  Length 32;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      4 ccaagggcgaatctca 19
          || |||| ||||||||
Db     15 CCCAGGGGGAATCTCA 30


RESULT  15
AX018574
LOCUS       AX018574       32 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 68 from Patent WO9945127.
ACCESSION   AX018574
VERSION     AX018574.1  GI:10042712
KEYWORDS    .
```

```
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kingsman,S.M., Mitrophanous,K., Patterson,A.V., Stratford,I.J.,
            Griffiths,L. and Kan,O.
  TITLE     Enhanced prodrug activation
  JOURNAL   Patent: WO 9945127-A 68 10-SEP-1999;
            KINGSMAN SUSAN MARY (GB); MITROPHANOUS KYRIACOS (GB); PATTERSON
            ADAM VORN (GB); STRATFORD IAN JAMES (GB); GRIFFITHS LEIGH (GB); KAN
            ON (GB); OXFORD BIOMEDICA LTD (GB)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="primer"
BASE COUNT        8 a      9 c      8 g      7 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 6;  Length 32;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       4 ccaagggcgaatctca 19
           || |||| ||||||||
Db      15 CCCAGGGGGAATCTCA 30


Search completed: March 13, 2002, 10:38:45
Job time: 4142 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 09:29:43 ; Search time 2671.52 Seconds
(without alignments)
123.504 Million cell updates/sec

Title: US-09-923-515-27
Perfect score: 20
Sequence: 1 tgtggtgtcatagaggacca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
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28: em_un:*
29: em_vi:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	15	75.0	15	6	I35245	I35245 Sequence 21
c 2	15	75.0	15	6	I35246	I35246 Sequence 21
c 3	15	75.0	15	6	I35247	I35247 Sequence 21
c 4	13.8	69.0	21	6	AX096074	AX096074 Sequence
5	13.8	69.0	51	6	AX165007	AX165007 Sequence
6	12.8	64.0	45	6	A22111	A22111 plasminogen
7	12.8	64.0	45	6	I45627	I45627 Sequence 9
c 8	12.8	64.0	48	6	A22082	A22082 oligonucleo
c 9	12.6	63.0	35	6	I40380	I40380 Sequence 13
c 10	12.6	63.0	42	6	AX074324	AX074324 Sequence
c 11	12.4	62.0	21	6	AR086022	AR086022 Sequence
c 12	12.4	62.0	21	6	AR086039	AR086039 Sequence
13	12.4	62.0	23	22	E11546	E11546 PCR primer
c 14	12.4	62.0	29	6	AR038878	AR038878 Sequence
15	12.4	62.0	29	6	AX119993	AX119993 Sequence
c 16	12.2	61.0	21	6	AR143681	AR143681 Sequence
17	12.2	61.0	21	6	AR143705	AR143705 Sequence
c 18	12.2	61.0	21	6	AR157255	AR157255 Sequence
19	12.2	61.0	21	6	AR157279	AR157279 Sequence
20	12.2	61.0	25	6	I25870	I25870 Sequence 2
c 21	12.2	61.0	27	10	MMM1294	X94894 M.musculus
22	12.2	61.0	34	6	AR016522	AR016522 Sequence
23	12.2	61.0	34	6	AR096905	AR096905 Sequence
24	12.2	61.0	39	6	AR139769	AR139769 Sequence
c 25	12.2	61.0	42	9	HUM13COL27	M68996 Human alpha
c 26	12.2	61.0	44	6	AR032543	AR032543 Sequence
c 27	12.2	61.0	44	6	I29283	I29283 Sequence 15
c 28	12.2	61.0	44	6	I90957	I90957 Sequence 15
c 29	12.2	61.0	57	9	H010868S07	AF321576 Homo sapi
c 30	12.2	61.0	57	9	AF084018	AF084018 Homo sapi
c 31	12.2	61.0	57	9	AF084025	AF084025 Homo sapi
c 32	12	60.0	15	6	I35244	I35244 Sequence 21
c 33	12	60.0	24	6	A48407	A48407 Sequence 30
c 34	12	60.0	24	6	AR008347	AR008347 Sequence
c 35	12	60.0	24	6	AR098247	AR098247 Sequence
c 36	12	60.0	29	6	AR122666	AR122666 Sequence
37	12	60.0	51	6	AX156849	AX156849 Sequence
38	12	60.0	51	6	AX156850	AX156850 Sequence
c 39	12	60.0	54	6	A41130	A41130 Sequence 27
40	12	60.0	58	9	S50868	S50868 TCR-J beta
c 41	11.8	59.0	15	6	I35260	I35260 Sequence 22
c 42	11.8	59.0	15	6	I35261	I35261 Sequence 22
c 43	11.8	59.0	20	6	AR126617	AR126617 Sequence
c 44	11.8	59.0	20	6	AX024458	AX024458 Sequence
45	11.8	59.0	20	6	AX024467	AX024467 Sequence

ALIGNMENTS

RESULT 1
I35245/c
LOCUS I35245 15 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 213 from patent US 5599706.
ACCESSION I35245
VERSION I35245.1 GI:2088213
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
TITLE Ribozymes targeted to apo(a) mRNA
JOURNAL Patent: US 5599706-A 213 04-FEB-1997;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
BASE COUNT 3 a 4 c 3 g 5 t
ORIGIN

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  Query Match             75.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 tgtcatagaggacca 20
          ||||||||||||||||
Db     15 TGTCATAGAGGACCA 1


RESULT   2
I35246/c
LOCUS       I35246         15 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 214 from patent US 5599706.
ACCESSION   I35246
VERSION     I35246.1  GI:2088214
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 214 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        3 a      4 c      3 g      5 t
ORIGIN


  Query Match             75.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 tgtcatagaggacca 20
          ||||||||||||||||
Db     15 TGTCATAGAGGACCA 1


RESULT   3
I35247/c
LOCUS       I35247         15 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 215 from patent US 5599706.
ACCESSION   I35247
VERSION     I35247.1  GI:2088215
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 215 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        3 a      6 c      2 g      4 t
ORIGIN


  Query Match             75.0%;  Score 15;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 ggtgtcatagaggac 18
          ||||||||||||||||
Db     15 GGTGTCATAGAGGAC 1


RESULT   4
AX096074/c
LOCUS       AX096074 .     21 bp    DNA             PAT       30-MAR-2001
DEFINITION  Sequence 1252 from Patent WO0118250.
ACCESSION   AX096074
VERSION     AX096074.1  GI:13512301
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
            Mccarthy,J.J.
  TITLE     Single nucleotide polymorphisms in genes
  JOURNAL   Patent: WO 0118250-A 1252 15-MAR-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
            Pharmaceuticals, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT        5 a      8 c      4 g      3 t      1 others
ORIGIN


  Query Match             69.0%;  Score 13.8;  DB 6;  Length 21;
  Best Local Similarity   78.9%;  Pred. No. 5.8e+03;
  Matches   15;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 gtggtgtcatagaggacca 20
          |||||||:|||  |  |||
Db     19 GTGGTGTCRTAGTGAGCCA 1


RESULT   5
AX165007
LOCUS       AX165007       51 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 202 from Patent WO0138586.
ACCESSION   AX165007
VERSION     AX165007.1  GI:14545836
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0138586-A 202 31-MAY-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     variation       26
                     /note="single nucleotide polymorphism
                     Accession number cg44924222"
BASE COUNT       10 a     13 c     18 g     10 t
ORIGIN


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  Best Local Similarity   88.2%;  Pred. No. 5.8e+03;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 tggtgtcatagaggacc 19
          ||||| |||| ||||||
Db     32 TGGTGGCATACAGGACC 48


RESULT   6
A22111
LOCUS       A22111         45 bp    DNA             PAT       30-SEP-1994
DEFINITION  plasminogen factor Xa analogue site sequence.
```

```
ACCESSION   A22111
VERSION     A22111.1  GI:641450
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   .
  TITLE     ACTIVATABLE FIBRINOLYTIC AND ANTI-THROMBOTIC PROTEINS
  JOURNAL   Patent: WO 9109118-A 33 27-JUN-1991;
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       11 a      3 c      22 g      9 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 6;  Length 45;
  Best Local Similarity   87.5%;  Pred. No. 2.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tgtggtgtcatagagg 16
          |||||||  |||||||
Db     10 TGTGGTGCAATAGAGG 25


RESULT   7
I45627
LOCUS       I45627         45 bp    DNA             PAT       07-OCT-1997
DEFINITION  Sequence 9 from patent US 5637492.
ACCESSION   I45627
VERSION     I45627.1  GI:2469729
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Dawson,K., Edwards,R.M. and Forman,J.M.
  TITLE     Activatable fibrinolytic and anti-thrombotic proteins
  JOURNAL   Patent: US 5637492-A 9 10-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="unknown"
BASE COUNT       11 a      3 c      22 g      9 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 6;  Length 45;
  Best Local Similarity   87.5%;  Pred. No. 2.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tgtggtgtcatagagg 16
          |||||||  |||||||
Db     10 TGTGGTGCAATAGAGG 25


RESULT   8
A22082/c
LOCUS       A22082         48 bp    DNA             PAT       29-SEP-1994
DEFINITION  oligonucleotide.
ACCESSION   A22082
VERSION     A22082.1  GI:641431
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   .
  TITLE     ACTIVATABLE FIBRINOLYTIC AND ANTI-THROMBOTIC PROTEINS
  JOURNAL   Patent: WO 9109118-A 9 27-JUN-1991;
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        8 a      25 c      3 g      12 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 6;  Length 48;
  Best Local Similarity   87.5%;  Pred. No. 2.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tgtggtgtcatagagg 16
          |||||||  |||||||
Db     33 TGTGGTGCAATAGAGG 18


RESULT   9
I40380/c
LOCUS       I40380         35 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 13 from patent US 5620892.
ACCESSION   I40380
VERSION     I40380.1  GI:2082672
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Kurtz,S.E., Knickerbocker,A.M. and McCullough,J.R.
  TITLE     Strain of Saccharomyces cerevisiae expressing the gene encoding
            potassium transporter minK
  JOURNAL   Patent: US 5620892-A 13 15-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
BASE COUNT       15 a      9 c      4 g      7 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 35;
  Best Local Similarity   78.9%;  Pred. No. 2.7e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 gtggtgtcatagaggacca 20
          ||||||| | | |||| ||
Db     35 GTGGTGTTAGACAGGATCA 17


RESULT  10
AX074324/c
LOCUS       AX074324       42 bp    DNA             PAT       06-FEB-2001
DEFINITION  Sequence 38 from Patent WO0104310.
ACCESSION   AX074324
VERSION     AX074324.1  GI:12710510
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 42)
  AUTHORS   Weber,E.R., Wood,K.V. and Hall,M.P.
  TITLE     Fc epsilon receptor-luminescence inducing protein chimeric nucleic
            acid molecules, fusion proteins and uses thereof
  JOURNAL   Patent: WO 0104310-A 38 18-JAN-2001;
            Heska Corporation (US) ; PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Primer"
BASE COUNT       12 a      12 c      11 g      7 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 42;
  Best Local Similarity   78.9%;  Pred. No. 2.8e+04;
```

```
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 tgtggtgtcatagaggacc 19
          | ||||||  |||||| ||
Db     20 TCTGGTGTTCTAGAGGGCC 2


RESULT  11
AR086022/c
LOCUS       AR086022       21 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 4 from patent US 5985547.
ACCESSION   AR086022
VERSION     AR086022.1  GI:10012788
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Mellins,E.D.
  TITLE     Detection of a mutation in the HLA-DM.beta. gene in an
            immunocompromised patient
  JOURNAL   Patent: US 5985547-A 4 16-NOV-1999;
FEATURES             Location/Qualifiers
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  Best Local Similarity   92.9%;  Pred. No. 3.5e+04;
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Qy      5 gtgtcatagaggac 18
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Db     14 GTGCCATAGAGGAC 1


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LOCUS       AR086039       21 bp    DNA             PAT       07-SEP-2000
DEFINITION  Sequence 21 from patent US 5985547.
ACCESSION   AR086039
VERSION     AR086039.1  GI:10012805
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Mellins,E.D.
  TITLE     Detection of a mutation in the HLA-DM.beta. gene in an
            immunocompromised patient
  JOURNAL   Patent: US 5985547-A 21 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
BASE COUNT        5 a      6 c      5 g      5 t
ORIGIN


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  Best Local Similarity   92.9%;  Pred. No. 3.5e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 gtgtcatagaggac 18
          ||| ||||||||||
Db     14 GTGCCATAGAGGAC 1


RESULT  13
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ID   E11546   standard; DNA; UNC; 23 BP.
XX
AC   E11546;
XX
SV   E11546.1
XX
DT   08-OCT-1997 (Rel. 52, Created)
DT   02-SEP-2000 (Rel. 65, Last updated, Version 2)
XX
DE   PCR primer to detect cytomegalovirus.
XX
KW   JP 1996163999-A/5.
XX
OS   unidentified
OC   unclassified.
XX
RN   [1]
RP   1-23
RA   Yamanishi K., Kondo M., Aono T., Yoshimoto M.;
RT   "OLIGONUCLEOTIDE FOR AMPLIFICATION AND DETECTION OF CYTOMEGALOVIRUS";
RL   Patent number JP1996163999-A/5, 25-JUN-1996.
RL   TOYOBO CO LTD.
XX
CC   OS   None
CC   OC   Artificial sequences.
CC   PN   JP 1996163999-A/5
CC   PD   25-JUN-1996
CC   PF   15-DEC-1994 JP 1994312029
CC   PI   YAMANISHI KOICHI, KONDO MOTOHIRO, AONO TOSHIYA,
CC   PI   YOSHIMOTO MISAO
CC   PC   C12Q1/68,C07H21/02,C07H21/04,C12N15/09,C12Q1/70;
CC   CC   strandedness: Single;
CC   CC   topology: Linear;
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CC   FH
CC   FT   source          1. .23
CC   FT                   /organism="Artificial sequences"
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FH   Key             Location/Qualifiers
FH
FT   source          1. .23
FT                   /db_xref="taxon:32644"
FT                   /organism="unidentified"
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  Best Local Similarity   92.9%;  Pred. No. 3.6e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tgtggtgtcataga 14
          |||||||| |||||
Db      7 TGTGGTGTGATAGA 20


RESULT  14
AR038878/c
LOCUS       AR038878       29 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 35 from patent US 5807703.
ACCESSION   AR038878
VERSION     AR038878.1  GI:5958241
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Jacobs,K., McCoy,J.M., LaVallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Evans,C., Spaulding,V. and Bowman,M.
  TITLE     Secreted proteins and polynucleotides encoding them
  JOURNAL   Patent: US 5807703-A 35 15-SEP-1998;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT        6 a      5 c      7 g     10 t      1 others
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ORIGIN

Query Match 62.0%; Score 12.4; DB 6; Length 29;
Best Local Similarity 92.9%; Pred. No. 3.6e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      29 GTCATACAGGACCA 16
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RESULT 15
AX119993
LOCUS AX119993 29 bp DNA PAT 11-MAY-2001
DEFINITION Sequence 15 from Patent WO0129217.
ACCESSION AX119993
VERSION AX119993.1 GI:14036727
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 29)
AUTHORS Prayaga,S.K., Taupier,R.J. and Bandaru,R.
TITLE Polypeptides and polynucleotides encoding same
JOURNAL Patent: WO 0129217-A 15 26-APR-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1. .29
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"
BASE COUNT 3 a 8 c 12 g 6 t
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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           |||||||||| ||
Db      12 TGGTGTCATAGCGG 25
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Job time: 4139 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 09:29:20 ; Search time 3124.31 Seconds
(without alignments)
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Title: US-09-923-515-17
Perfect score: 20
Sequence: 1 ttctgcgtctgagcattgcg 20

Scoring table: IDENTITY_NUC
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Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
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33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
c 1	15	75.0	15	6	I35043	I35043 Sequence 11
c 2	14.2	71.0	28	6	A83871	A83871 Sequence 6
3	12.8	64.0	21	12	AB068595	AB068595 Synthetic
4	12.8	64.0	36	6	AX077289	AX077289 Sequence
5	12.6	63.0	20	6	AR068792	AR068792 Sequence
6	12.6	63.0	20	6	AR092666	AR092666 Sequence
7	12.6	63.0	20	6	AR130996	AR130996 Sequence
8	12.6	63.0	21	6	AX046113	AX046113 Sequence
c 9	12.6	63.0	28	6	A83872	A83872 Sequence 7
10	12.6	63.0	36	6	AX137165	AX137165 Sequence
c 11	12.6	63.0	36	6	AX137166	AX137166 Sequence
c 12	12.6	63.0	37	6	I43879	I43879 Sequence 14
c 13	12.6	63.0	51	6	AX157429	AX157429 Sequence
c 14	12.6	63.0	51	6	AX157430	AX157430 Sequence
15	12.6	63.0	51	6	AX158420	AX158420 Sequence
c 16	12.6	63.0	51	6	AX160028	AX160028 Sequence
17	12.4	62.0	20	6	AR031058	AR031058 Sequence
18	12.4	62.0	20	6	AR043298	AR043298 Sequence
19	12.4	62.0	20	6	AR074953	AR074953 Sequence
20	12.4	62.0	20	6	I82149	I82149 Sequence 86
21	12.4	62.0	60	6	AR043215	AR043215 Sequence
22	12.4	62.0	60	6	AR074870	AR074870 Sequence
23	12.4	62.0	60	6	I82066	I82066 Sequence 3
c 24	12.2	61.0	17	6	E00666	E00666 Oligonucleo
c 25	12.2	61.0	17	6	E00675	E00675 Oligonucleo
c 26	12.2	61.0	17	6	E00681	E00681 Oligonucleo
27	12.2	61.0	20	12	AB069376	AB069376 Synthetic
c 28	12.2	61.0	27	6	AR039372	AR039372 Sequence
c 29	12.2	61.0	45	6	AR088052	AR088052 Sequence
c 30	12	60.0	19	6	AR089051	AR089051 Sequence
c 31	12	60.0	19	6	AR140687	AR140687 Sequence
c 32	12	60.0	22	6	I77122	I77122 Sequence 8
c 33	12	60.0	25	6	I43029	I43029 Sequence 12
c 34	12	60.0	43	6	AX011025	AX011025 Sequence
c 35	12	60.0	50	6	AR032644	AR032644 Sequence
c 36	12	60.0	50	6	AR032654	AR032654 Sequence
c 37	12	60.0	50	6	I29384	I29384 Sequence 25
c 38	12	60.0	50	6	I29394	I29394 Sequence 26
c 39	12	60.0	50	6	I43028	I43028 Sequence 11
c 40	12	60.0	50	6	I91058	I91058 Sequence 25
c 41	12	60.0	50	6	I91068	I91068 Sequence 26
42	12	60.0	51	6	AX157994	AX157994 Sequence
c 43	11.8	59.0	15	6	I35061	I35061 Sequence 29
c 44	11.8	59.0	15	6	I35108	I35108 Sequence 76
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ALIGNMENTS

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DEFINITION Sequence 11 from patent US 5599706.
ACCESSION I35043
VERSION I35043.1 GI:2088011
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
TITLE Ribozymes targeted to apo(a) mRNA
JOURNAL Patent: US 5599706-A 11-04-FEB-1997;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
BASE COUNT 5 a 5 c 3 g 2 t
ORIGIN

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 tgcgtctgagcattg 18
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Db     15 TGCGTCTGAGCATTG 1


RESULT   2
A83871/c
LOCUS       A83871          28 bp    DNA             PAT       21-JAN-2000
DEFINITION  Sequence 6 from Patent WO9848018.
ACCESSION   A83871
VERSION     A83871.1  GI:6733041
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Schneider-Fresenius,C. and Otto,B.
  TITLE     RECOMBINANT HUMAN BETA INTERFERON WITH ENHANCED SOLUBILITY
  JOURNAL   Patent: WO 9848018-A 6 29-OCT-1998;
            SCHNEIDER FRESENIUS CHRISTIAN (DE); OTTO BERND (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32644"
BASE COUNT        8 a      10 c       5 g       5 t
ORIGIN


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Qy      1 ttctgcgtctgagcattgc 19
          ||||| | ||||| |||||
Db     23 TTCTGGGACTGAGAATTGC 5


RESULT   3
AB068595
LOCUS       AB068595        21 bp    DNA             SYN       08-AUG-2001
DEFINITION  Synthetic construct DNA, reverse primer for human STS sts-stSG27932
            at 1p36.
ACCESSION   AB068595
VERSION     AB068595.1  GI:15129399
KEYWORDS    .
SOURCE      synthetic construct DNA.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A bac-based sts-content map spanning a 35-mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics. 74 (1), 55-70 (2001)
  MEDLINE   21269192
REFERENCE   2  (bases 1 to 21)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail.horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
     misc_feature    1. .21
                     /note="reverse primer for human STS sts-stSG27932 at 1p36
                     sts-stSG27932 obtained from clones B72G3, B370L16,
                     B341F17, B265D10, B341F17, B53F6, B128O2, B85K5, B73C3,
                     Human BAC library RPCI-11"
BASE COUNT        2 a      7 c       4 g       8 t
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  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 tctgcgtctgagcatt 17
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Db      2 TCTCCGTCTGACCATT 17


RESULT   4
AX077289
LOCUS       AX077289        36 bp    DNA             PAT       22-FEB-2001
DEFINITION  Sequence 4 from Patent WO0105808.
ACCESSION   AX077289
VERSION     AX077289.1  GI:13121876
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Nygren,P., Uhlen,M. and Nord,O.
  TITLE     In vitro selection and optional identification of polypeptides
            using solid support carriers
  JOURNAL   Patent: WO 0105808-A 4 25-JAN-2001;
            Affibody Technology Sweden AB (SE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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ORIGIN


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  Best Local Similarity   87.5%;  Pred. No. 3.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 ttctgcgtctgagcat 16
          ||| ||| ||||||||
Db     18 TTCGGCGCCTGAGCAT 33


RESULT   5
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LOCUS       AR068792        20 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 23 from patent US 5854050.
ACCESSION   AR068792
VERSION     AR068792.1  GI:6000999
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dalb.o slashed.ge,H., Christgau,S., Andersen,L.Nonboe,
            Kofod,L.Venke, Kauppinen,M.Sakari, Nielsen,J.Bech and Dambmann,C.
  TITLE     Enzyme with protease activity
  JOURNAL   Patent: US 5854050-A 23 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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(without alignments)
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Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
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21: em_ov:*
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26: em_sts:*
27: em_sy:*
28: em_un:*
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32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.		Score	Query Match	Length	DB	ID	Description
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c	3	14.4	72.0	16	6	I35407	I35407 Sequence 37
c	4	14.4	72.0	16	6	I35415	I35415 Sequence 38
c	5	13.4	67.0	15	6	I35197	I35197 Sequence 16
c	6	13.4	67.0	15	6	I35198	I35198 Sequence 16
c	7	13.4	67.0	15	6	I35199	I35199 Sequence 16
c	8	13.4	67.0	16	6	I35406	I35406 Sequence 37
c	9	13.4	67.0	16	6	I35414	I35414 Sequence 38
	10	13.2	66.0	27	6	A27233	A27233 CAT-Poliovi
c	11	13.2	66.0	37	9	AB055779	AB055779 Homo sapi
c	12	12.8	64.0	16	6	I35411	I35411 Sequence 37
c	13	12.8	64.0	23	6	A04043	A04043 Synthetic o
	14	12.8	64.0	50	6	AR099999	AR099999 Sequence
	15	12.6	63.0	37	6	AR019520	AR019520 Sequence
c	16	12.2	61.0	37	6	AX185857	AX185857 Sequence
c	17	12.2	61.0	45	6	AR032679	AR032679 Sequence
c	18	12.2	61.0	45	6	I29419	I29419 Sequence 29
c	19	12.2	61.0	45	6	I91093	I91093 Sequence 29
c	20	12.2	61.0	47	9	HUMRPS	D28348 Human mRNA
c	21	12.2	61.0	48	6	AR004898	AR004898 Sequence
c	22	12.2	61.0	48	6	AR020580	AR020580 Sequence
	23	12.2	61.0	48	6	AX068205	AX068205 Sequence
	24	12.2	61.0	48	6	AX068206	AX068206 Sequence
	25	12.2	61.0	48	6	AX068208	AX068208 Sequence
	26	12.2	61.0	48	6	AX068209	AX068209 Sequence
	27	12.2	61.0	48	6	AX068210	AX068210 Sequence
c	28	12.2	61.0	51	6	AX157685	AX157685 Sequence
c	29	12.2	61.0	51	6	AX157687	AX157687 Sequence
c	30	12.2	61.0	51	6	AX157688	AX157688 Sequence
	31	12	60.0	20	6	AR118886	AR118886 Sequence
c	32	12	60.0	29	6	AR034318	AR034318 Sequence
c	33	12	60.0	29	6	AR034320	AR034320 Sequence
c	34	12	60.0	29	6	AR035424	AR035424 Sequence
c	35	12	60.0	29	6	AR035426	AR035426 Sequence
c	36	12	60.0	29	6	AR050839	AR050839 Sequence
c	37	12	60.0	29	6	AR050841	AR050841 Sequence
c	38	12	60.0	29	6	AR053844	AR053844 Sequence
c	39	12	60.0	29	6	AR053846	AR053846 Sequence
c	40	12	60.0	29	6	AR091625	AR091625 Sequence
c	41	12	60.0	29	6	AR091627	AR091627 Sequence
c	42	12	60.0	29	6	AR117504	AR117504 Sequence
c	43	12	60.0	29	6	AR117506	AR117506 Sequence
c	44	12	60.0	45	10	S77072	S77072 T-cell rece
c	45	12	60.0	50	6	AX093080	AX093080 Sequence

ALIGNMENTS

RESULT 1
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LOCUS I35370 16 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 338 from patent US 5599706.
ACCESSION I35370
VERSION I35370.1 GI:2088338
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
TITLE Ribozymes targeted to apo(a) mRNA
JOURNAL Patent: US 5599706-A 338 04-FEB-1997;
FEATURES Location/Qualifiers
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BASE COUNT 0 a 9 c 4 g 3 t
ORIGIN

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Db     16 GGAGGCGCGACGGCAG 1


RESULT   2
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LOCUS       I35369         16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 337 from patent US 5599706.
ACCESSION   I35369
VERSION     I35369.1  GI:2088337
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 337 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        1 a      7 c      6 g      2 t
ORIGIN


  Query Match             75.0%;  Score 15;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+04;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      6 ggcgcgacggcagtc 20
          |||||||||||||||
Db     16 GGCGCGACGGCAGTC 2


RESULT   3
I35407/c
LOCUS       I35407         16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 375 from patent US 5599706.
ACCESSION   I35407
VERSION     I35407.1  GI:2088375
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 375 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        1 a      9 c      3 g      3 t
ORIGIN


  Query Match             72.0%;  Score 14.4;  DB 6;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.7e+04;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 ggaggcgcgacggcag 18
          ||||| ||||||||||
Db     16 GGAGGTGCGACGGCAG 1


RESULT   4
I35415/c
LOCUS       I35415         16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 383 from patent US 5599706.
ACCESSION   I35415
VERSION     I35415.1  GI:2088383
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 383 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        1 a      9 c      3 g      3 t
ORIGIN


  Query Match             72.0%;  Score 14.4;  DB 6;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.7e+04;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 ggaggcgcgacggcag 18
          ||||| ||||||||||
Db     16 GGAGGTGCGACGGCAG 1


RESULT   5
I35197/c
LOCUS       I35197         15 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 165 from patent US 5599706.
ACCESSION   I35197
VERSION     I35197.1  GI:2088165
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 165 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        1 a      8 c      3 g      3 t
ORIGIN


  Query Match             67.0%;  Score 13.4;  DB 6;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 gaggcgcgacggcag 18
          |||| ||||||||||
Db     15 GAGGTGCGACGGCAG 1


RESULT   6
I35198/c
LOCUS       I35198         15 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 166 from patent US 5599706.
ACCESSION   I35198
VERSION     I35198.1  GI:2088166
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 166 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .15
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  Query Match             63.0%;  Score 12.6;  DB 6;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.1e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ttctgcgtctgagcattgc 19
          ||||| |||||| ||  ||
Db      2 TTCTGGGTCTGACCACCGC 20


RESULT   6
AR092666
LOCUS       AR092666       20 bp    DNA             PAT       08-SEP-2000
DEFINITION  Sequence 23 from patent US 5998190.
ACCESSION   AR092666
VERSION     AR092666.1  GI:10019418
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dalb.o slashed.ge,H., Christgau,S., Andersen,L.Nonboe,
            Kofod,L.Venke, Kauppinen,M.Sakari, Nielsen,J.Bech and Dambmann,C.
  TITLE     Enzyme with protease activity
  JOURNAL   Patent: US 5998190-A 23 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        2 a      8 c      5 g      5 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.1e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ttctgcgtctgagcattgc 19
          ||||| |||||| ||  ||
Db      2 TTCTGGGTCTGACCACCGC 20


RESULT   7
AR130996
LOCUS       AR130996       20 bp    DNA             PAT       16-MAY-2001
DEFINITION  Sequence 23 from patent US 6190905.
ACCESSION   AR130996
VERSION     AR130996.1  GI:14119321
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dalb.o slashed.ge,H., Christgau,S., Andersen,L.Nonboe,
            Kofod,L.Venke, Kauppinen,M.Sakari, Nielsen,J.Bech and Dambmann,C.
  TITLE     Enzyme with protease activity
  JOURNAL   Patent: US 6190905-A 23 20-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
BASE COUNT        2 a      8 c      5 g      5 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 4.1e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ttctgcgtctgagcattgc 19
          ||||| |||||| ||  ||
Db      2 TTCTGGGTCTGACCACCGC 20


RESULT   8
AX046113
LOCUS       AX046113       21 bp    DNA             PAT       24-NOV-2000
DEFINITION  Sequence 2 from Patent WO0066725.
ACCESSION   AX046113
VERSION     AX046113.1  GI:11344214
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Parmentier,S., Bohme,A. and Plotkine,M.
  TITLE     Use of inducible no-synthase antisense oligonucleotides for
            preventing and treating cerebral ischemia
  JOURNAL   Patent: WO 0066725-A 2 09-NOV-2000;
            Aventis Pharma S.A. (FR)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide antisens de iNOS"
BASE COUNT        3 a      7 c      4 g      7 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 21;
  Best Local Similarity   78.9%;  Pred. No. 4.1e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ttctgcgtctgagcattgc 19
          ||| | |||||  ||||||
Db      2 TTCAGAGTCTGCCCATTGC 20


RESULT   9
A83872/c
LOCUS       A83872         28 bp    DNA             PAT       21-JAN-2000
DEFINITION  Sequence 7 from Patent WO9848018.
ACCESSION   A83872
VERSION     A83872.1  GI:6733042
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Schneider-Fresenius,C. and Otto,B.
  TITLE     RECOMBINANT HUMAN BETA INTERFERON WITH ENHANCED SOLUBILITY
  JOURNAL   Patent: WO 9848018-A 7 29-OCT-1998;
            SCHNEIDER FRESENIUS CHRISTIAN (DE); OTTO BERND (DE)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT        8 a      9 c      5 g      6 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 28;
  Best Local Similarity   78.9%;  Pred. No. 4e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ttctgcgtctgagcattgc 19
          ||||| | ||||  |||||
Db     23 TTCTGGGACTGAAAATTGC 5


RESULT  10
AX137165
LOCUS       AX137165       36 bp    DNA             PAT       30-MAY-2001
DEFINITION  Sequence 16 from Patent EP1092764.
ACCESSION   AX137165
VERSION     AX137165.1  GI:14273491
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
```

```
            artificial sequence.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Bartok,A., Mueh,T. and Rueckel,M.
  TITLE     Continuous fermentation process
  JOURNAL   Patent: EP 1092764-A 16 18-APR-2001;
            F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT        7 a     11 c      6 g     12 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 36;
  Best Local Similarity   78.9%;  Pred. No. 4e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

 y      1 ttctgcgtctgagcattgc 19
          |||||||||| ||  || |
Db     14 TTCTGCGTCTAAGGCTTAC 32


RESULT  11
AX137166/c
LOCUS       AX137166        36 bp    DNA             PAT       30-MAY-2001
DEFINITION  Sequence 17 from Patent EP1092764.
ACCESSION   AX137166
VERSION     AX137166.1  GI:14273492
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Bartok,A., Mueh,T. and Rueckel,M.
  TITLE     Continuous fermentation process
  JOURNAL   Patent: EP 1092764-A 17 18-APR-2001;
            F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Primer"
BASE COUNT       12 a      6 c     11 g      7 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 36;
  Best Local Similarity   78.9%;  Pred. No. 4e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ttctgcgtctgagcattgc 19
          |||||||||| ||  || |
Db     23 TTCTGCGTCTAAGGCTTAC 5


RESULT  12
I43879/c
LOCUS       I43879          37 bp    DNA             PAT       07-OCT-1997
DEFINITION  Sequence 14 from patent US 5633227.
ACCESSION   I43879
VERSION     I43879.1  GI:2468977
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Muller,D.K., Brownell,E. and Delaria,K.A.
  TITLE     Secretory leukocyte protease inhibitor as an inhibitor of tryptase
  JOURNAL   Patent: US 5633227-A 14 27-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="unknown"
BASE COUNT       10 a      9 c     11 g      7 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 37;
  Best Local Similarity   78.9%;  Pred. No. 4e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ttctgcgtctgagcattgc 19
          | |||||| |||| ||| |
Db     24 TCCTGCGTTTGAGAATTCC 6


RESULT  13
AX157429/c
LOCUS       AX157429        51 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 757 from Patent WO0140521.
ACCESSION   AX157429
VERSION     AX157429.1  GI:14538760
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 757 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="1 of 2 allelic variants (758 is other entry)
                     Accession number cg21428762"
BASE COUNT       15 a     11 c     19 g      6 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 51;
  Best Local Similarity   78.9%;  Pred. No. 4e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 tctgcgtctgagcattgcg 20
          |||||||| |||||   ||
Db     41 TCTGCGTCCGAGCACCCCG 23


RESULT  14
AX157430/c
LOCUS       AX157430        51 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 758 from Patent WO0140521.
ACCESSION   AX157430
VERSION     AX157430.1  GI:14538761
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 758 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    26
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```
                     /note="2 of 2 allelic variants (757 is other entry)
                     Accession number cg21428762"
BASE COUNT       15 a     11 c     18 g      7 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 51;
  Best Local Similarity   78.9%;  Pred. No. 4e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 tctgcgtctgagcattgcg 20
          |||||||| |||||   ||
Db     41 TCTGCGTCCGAGCACACCG 23


RESULT  15
AX158420
LOCUS       AX158420       51 bp    DNA             PAT       22-JUN-2001
DEFINITION  Sequence 1748 from Patent WO0140521.
ACCESSION   AX158420
VERSION     AX158420.1  GI:14539751
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 1748 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     misc_feature    26
                     /note="2 of 2 allelic variants (1747 is other entry)
                     Accession number cg34407558"
BASE COUNT       10 a     15 c      9 g     17 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 51;
  Best Local Similarity   78.9%;  Pred. No. 4e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 ttctgcgtctgagcattgc 19
          || || | |||||||||| |
Db     12 TTTTGAGGCTGAGCATTTC 30


Search completed: March 13, 2002, 09:29:21
Job time: 3871 sec
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                     /organism="unknown"
BASE COUNT        1 a      8 c      3 g      3 t
ORIGIN


  Query Match             67.0%;  Score 13.4;  DB 6;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 gaggcgcgacggcag 18
          |||| ||||||||||
Db     15 GAGGTGCGACGGCAG 1


RESULT   7
I35199/c
LOCUS       I35199         15 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 167 from patent US 5599706.
ACCESSION   I35199
VERSION     I35199.1  GI:2088167
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 167 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        1 a      8 c      3 g      3 t
ORIGIN


  Query Match             67.0%;  Score 13.4;  DB 6;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      4 gaggcgcgacggcag 18
          |||| ||||||||||
Db     15 GAGGTGCGACGGCAG 1


RESULT   8
I35406/c
LOCUS       I35406         16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 374 from patent US 5599706.
ACCESSION   I35406
VERSION     I35406.1  GI:2088374
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 374 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        2 a      7 c      5 g      2 t
ORIGIN


  Query Match             67.0%;  Score 13.4;  DB 6;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      6 ggcgcgacggcagtc 20
          || ||||||||||||
Db     16 GGTGCGACGGCAGTC 2


RESULT   9
I35414/c
LOCUS       I35414         16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 382 from patent US 5599706.
ACCESSION   I35414
VERSION     I35414.1  GI:2088382
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 382 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        2 a      7 c      5 g      2 t
ORIGIN


  Query Match             67.0%;  Score 13.4;  DB 6;  Length 16;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      6 ggcgcgacggcagtc 20
          || ||||||||||||
Db     16 GGTGCGACGGCAGTC 2


RESULT  10
A27233
LOCUS       A27233         27 bp    DNA             PAT       27-SEP-1995
DEFINITION  CAT-Poliovirus gene C-terminal fusion.
ACCESSION   A27233
VERSION     A27233.1  GI:1248395
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   .
  JOURNAL   Patent: GB 2262099-A 10 09-JUN-1993;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
     CDS             <1. .>27
                     /note="sequence at C-terminal CAT-Polio fusion"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAA01859.1"
                     /db_xref="GI:1248396"
                     /translation="QGGATSDNL"
BASE COUNT        8 a      8 c      8 g      3 t
ORIGIN


  Query Match             66.0%;  Score 13.2;  DB 6;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+05;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      3 ggaggcgcgacggcagtc 20
          ||||| |||||| ||| |
Db      4 GGAGGTGCGACGTCAGAC 21


RESULT  11
AB055779/c
LOCUS       AB055779       37 bp    mRNA            PRI       14-AUG-2001
DEFINITION  Homo sapiens mRNA for ribosomal protein S28, partial cds.
ACCESSION   AB055779
```

```
VERSION     AB055779.1  GI:15149551
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone:HP00599.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kato,S.
  TITLE     Human mRNA for ribosomal protein L5, 5'UTR (sequence from the 5'
            cap to the start codon)
  JOURNAL   Published Only in Database (2001) In press
REFERENCE   2  (bases 1 to 37)
  AUTHORS   Kato,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-2001) Seishi Kato, Sagami Chemical Research
            Center, Genetic Engineering Section; 4-4-1 Nishi-Ohnuma,
            Sagamihara, Kanagawa 229-0012, Japan (E-mail:seishi@sagami.ne.jp,
            Tel:81-42-742-4791, Fax:81-42-749-7631)
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="HP00599"
     5'UTR           1. .31
     CDS             32. .>37
                     /codon_start=1
                     /product="ribosomal protein S28"
                     /protein_id="BAB62873.1"
                     /db_xref="GI:15149552"
                     /translation="MD"
BASE COUNT        5 a      19 c       9 g       4 t
ORIGIN


  Query Match             66.0%;  Score 13.2;  DB 9;  Length 37;
  Best Local Similarity   83.3%;  Pred. No. 1.3e+05;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      3 ggaggcgcgacggcagtc 20
          || |||||| |||| |||
Db     28 GGCGGCGCGGCGGCGGTC 11


RESULT  12
I35411/c
LOCUS       I35411         16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 379 from patent US 5599706.
ACCESSION   I35411
VERSION     I35411.1  GI:2088379
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 379 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        2 a       8 c       3 g       3 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 6;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 ggaggcgcgacggcag 18
          ||||| ||||| ||||
Db     16 GGAGGTGCGACTGCAG 1


RESULT  13
A04043/c
LOCUS       A04043         23 bp    DNA             PAT       04-JUN-1993
DEFINITION  Synthetic oligonucleotide.
ACCESSION   A04043
VERSION     A04043.1  GI:412381
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   .
  TITLE     tPA-LIKE POLYPEPTIDES, THEIR MANUFACTURE AND USE
  JOURNAL   Patent: WO 9003436-A 13 05-APR-1990;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        1 a       13 c       5 g       4 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 6;  Length 23;
  Best Local Similarity   87.5%;  Pred. No. 2.3e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 cggaggcgcgacggca 17
          |||||| | |||||||
Db     18 CGGAGGGGAGACGGCA 3


RESULT  14
AR099999
LOCUS       AR099999       50 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 25 from patent US 6080543.
ACCESSION   AR099999
VERSION     AR099999.1  GI:12810447
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Engel,S.R., Descenzo,R.A. and Irelan,N.A.
  TITLE     Detection of fungal pathogens
  JOURNAL   Patent: US 6080543-A 25 27-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="unknown"
BASE COUNT        9 a       15 c       17 g       9 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 6;  Length 50;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps.   0;

Qy      4 gaggcgcgacggcagt 19
          |||||||| | |||||
Db     12 GAGGCGCGTCCGCAGT 27


RESULT  15
AR019520
LOCUS       AR019520       37 bp    DNA             PAT       05-DEC-1998
DEFINITION  Sequence 9 from patent US 5783665.
ACCESSION   AR019520
VERSION     AR019520.1  GI:3974634
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Baum,P.R., Fanslow,W.C. III, Gayle,R.B. and Goodwin,R.G.
```

```
  TITLE     Cytokine which is a ligand for OX40
  JOURNAL   Patent: US 5783665-A 9 21-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="unknown"
BASE COUNT        6 a     15 c     11 g      5 t
ORIGIN


  Query Match             63.0%;  Score 12.6;  DB 6;  Length 37;
  Best Local Similarity   78.9%;  Pred. No. 2.5e+05;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2 cggaggcgcgacggcagtc 20
           ||  |||||| || |||||
Db      15 CGAGGGCGCGCCGTCAGTC 33


Search completed: March 13, 2002, 09:29:11
Job time: 3861 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 13, 2002, 09:29:11 ; Search time 3124.31 Seconds
(without alignments)
105.605 Million cell updates/sec

Title: US-09-923-515-11
Perfect score: 20
Sequence: 1 cggaggcgcgacggcagtcc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
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24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vi:*
30: em_htgo_hum:*
31: em_htgo_inv:*
32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.		Score	Query Match	Length	DB	ID	Description
c	1	16	80.0	16	6	I35369	I35369 Sequence 33
c	2	16	80.0	16	6	I35370	I35370 Sequence 33
c	3	14.4	72.0	16	6	I35406	I35406 Sequence 37
c	4	14.4	72.0	16	6	I35407	I35407 Sequence 37
c	5	14.4	72.0	16	6	I35414	I35414 Sequence 38
c	6	14.4	72.0	16	6	I35415	I35415 Sequence 38
c	7	13.4	67.0	15	6	I35197	I35197 Sequence 16
c	8	13.4	67.0	15	6	I35198	I35198 Sequence 16
c	9	13.4	67.0	15	6	I35199	I35199 Sequence 16
	10	13.2	66.0	27	6	A27233	A27233 CAT-Poliovi
c	11	13.2	66.0	37	9	AB055779	AB055779 Homo sapi
c	12	12.8	64.0	16	6	I35411	I35411 Sequence 37
c	13	12.8	64.0	23	6	A04043	A04043 Synthetic o
	14	12.8	64.0	50	6	AR099999	AR099999 Sequence
	15	12.8	64.0	52	6	I35351	I35351 Sequence 31
c	16	12.6	63.0	19	6	AX130668	AX130668 Sequence
	17	12.6	63.0	24	6	AX061528	AX061528 Sequence
c	18	12.6	63.0	36	4	PIGAMPU	M60006 S.scrofa SI
	19	12.6	63.0	37	6	AR019520	AR019520 Sequence
	20	12.6	63.0	48	6	AX068205	AX068205 Sequence
	21	12.6	63.0	48	6	AX068206	AX068206 Sequence
	22	12.6	63.0	48	6	AX068208	AX068208 Sequence
	23	12.6	63.0	48	6	AX068209	AX068209 Sequence
	24	12.6	63.0	48	6	AX068210	AX068210 Sequence
c	25	12.6	63.0	52	6	A33450	A33450 Synthetic H
c	26	12.6	63.0	59	6	AR075431	AR075431 Sequence
c	27	12.6	63.0	59	6	AR107508	AR107508 Sequence
	28	12.2	61.0	21	6	AR130949	AR130949 Sequence
	29	12.2	61.0	21	6	I91932	I91932 Sequence 5
	30	12.2	61.0	24	6	AR090844	AR090844 Sequence
c	31	12.2	61.0	37	6	AX185857	AX185857 Sequence
c	32	12.2	61.0	45	6	AR032679	AR032679 Sequence
c	33	12.2	61.0	45	6	I29419	I29419 Sequence 29
c	34	12.2	61.0	45	6	I91093	I91093 Sequence 29
c	35	12.2	61.0	51	6	AX157685	AX157685 Sequence
c	36	12.2	61.0	51	6	AX157687	AX157687 Sequence
c	37	12.2	61.0	51	6	AX157688	AX157688 Sequence
c	38	12	60.0	21	6	AR074278	AR074278 Sequence
c	39	12	60.0	21	6	AX032640	AX032640 Sequence
c	40	12	60.0	34	9	S80689	S80689 gamma delta
c	41	12	60.0	34	9	S80843	S80843 gamma delta
c	42	12	60.0	44	6	AR002174	AR002174 Sequence
	43	12	60.0	48	6	A50986	A50986 Sequence 27
c	44	12	60.0	48	6	A50987	A50987 Sequence 28
	45	12	60.0	49	6	AX002730	AX002730 Sequence

ALIGNMENTS

RESULT 1
I35369/c
LOCUS I35369 16 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 337 from patent US 5599706.
ACCESSION I35369
VERSION I35369.1 GI:2088337
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
TITLE Ribozymes targeted to apo(a) mRNA
JOURNAL Patent: US 5599706-A 337 04-FEB-1997;
FEATURES Location/Qualifiers
source 1. .16
/organism="unknown"
BASE COUNT 1 a 7 c 6 g 2 t
ORIGIN

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  Query Match             80.0%;  Score 16;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 ggcgcgacggcagtcc 20
          ||||||||||||||||
Db     16 GGCGCGACGGCAGTCC 1


RESULT   2
I35370/c
LOCUS       I35370         16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 338 from patent US 5599706.
ACCESSION   I35370
VERSION     I35370.1  GI:2088338
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
 EFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 338 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        0 a      9 c      4 g      3 t
ORIGIN


  Query Match             80.0%;  Score 16;  DB 6;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+03;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ggaggcgcgacggcag 17
          ||||||||||||||||
Db     16 GGAGGCGCGACGGCAG 1


RESULT   3
I35406/c
LOCUS       I35406         16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 374 from patent US 5599706.
ACCESSION   I35406
VERSION     I35406.1  GI:2088374
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 374 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        2 a      7 c      5 g      2 t
ORIGIN


  Query Match             72.0%;  Score 14.4;  DB 6;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.9e+04;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 ggcgcgacggcagtcc 20
          || |||||||||||||
Db     16 GGTGCGACGGCAGTCC 1


RESULT   4
I35407/c
LOCUS       I35407         16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 375 from patent US 5599706.
ACCESSION   I35407
VERSION     I35407.1  GI:2088375
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 375 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        1 a      9 c      3 g      3 t
ORIGIN


  Query Match             72.0%;  Score 14.4;  DB 6;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.9e+04;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ggaggcgcgacggcag 17
          ||||| ||||||||||
Db     16 GGAGGTGCGACGGCAG 1


RESULT   5
I35414/c
LOCUS       I35414         16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 382 from patent US 5599706.
ACCESSION   I35414
VERSION     I35414.1  GI:2088382
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 382 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        2 a      7 c      5 g      2 t
ORIGIN


  Query Match             72.0%;  Score 14.4;  DB 6;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.9e+04;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      5 ggcgcgacggcagtcc 20
          || |||||||||||||
Db     16 GGTGCGACGGCAGTCC 1


RESULT   6
I35415/c
LOCUS       I35415         16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 383 from patent US 5599706.
ACCESSION   I35415
VERSION     I35415.1  GI:2088383
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 383 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
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                     /organism="unknown"
BASE COUNT        1 a      9 c      3 g      3 t
ORIGIN


  Query Match             72.0%;  Score 14.4;  DB 6;  Length 16;
  Best Local Similarity   93.8%;  Pred. No. 4.9e+04;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      2 ggaggcgcgacggcag 17
          ||||| ||||||||||
Db     16 GGAGGTGCGACGGCAG 1


RESULT   7
I35197/c
LOCUS       I35197         15 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 165 from patent US 5599706.
ACCESSION   I35197
VERSION     I35197.1  GI:2088165
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 165 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        1 a      8 c      3 g      3 t
ORIGIN


  Query Match             67.0%;  Score 13.4;  DB 6;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 gaggcgcgacggcag 17
          |||| ||||||||||
Db     15 GAGGTGCGACGGCAG 1


RESULT   8
I35198/c
LOCUS       I35198         15 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 166 from patent US 5599706.
ACCESSION   I35198
VERSION     I35198.1  GI:2088166
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 166 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        1 a      8 c      3 g      3 t
ORIGIN


  Query Match             67.0%;  Score 13.4;  DB 6;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 gaggcgcgacggcag 17
          |||| ||||||||||
Db     15 GAGGTGCGACGGCAG 1


RESULT   9
I35199/c
LOCUS       I35199         15 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 167 from patent US 5599706.
ACCESSION   I35199
VERSION     I35199.1  GI:2088167
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 167 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
BASE COUNT        1 a      8 c      3 g      3 t
ORIGIN


  Query Match             67.0%;  Score 13.4;  DB 6;  Length 15;
  Best Local Similarity   93.3%;  Pred. No. 1.4e+05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      3 gaggcgcgacggcag 17
          |||| ||||||||||
Db     15 GAGGTGCGACGGCAG 1


RESULT  10
A27233
LOCUS       A27233         27 bp    DNA             PAT       27-SEP-1995
DEFINITION  CAT-Poliovirus gene C-terminal fusion.
ACCESSION   A27233
VERSION     A27233.1  GI:1248395
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   .
  JOURNAL   Patent: GB 2262099-A 10 09-JUN-1993;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
     CDS             <1. .>27
                     /note="sequence at C-terminal CAT-Polio fusion"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAA01859.1"
                     /db_xref="GI:1248396"
                     /translation="QGGATSDNL"
BASE COUNT        8 a      8 c      8 g      3 t
ORIGIN


  Query Match             66.0%;  Score 13.2;  DB 6;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+05;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 ggaggcgcgacggcagtc 19
          ||||| |||||| ||| |
Db      4 GGAGGTGCGACGTCAGAC 21


RESULT  11
AB055779/c
LOCUS       AB055779       37 bp    mRNA            PRI       14-AUG-2001
DEFINITION  Homo sapiens mRNA for ribosomal protein S28, partial cds.
ACCESSION   AB055779
```

```
VERSION     AB055779.1  GI:15149551
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone:HP00599.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Kato,S.
  TITLE     Human mRNA for ribosomal protein L5, 5'UTR (sequence from the 5'
            cap to the start codon)
  JOURNAL   Published Only in Database (2001) In press
REFERENCE   2  (bases 1 to 37)
  AUTHORS   Kato,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-2001) Seishi Kato, Sagami Chemical Research
            Center, Genetic Engineering Section; 4-4-1 Nishi-Ohnuma,
            Sagamihara, Kanagawa 229-0012, Japan (E-mail:seishi@sagami.ne.jp,
            Tel:81-42-742-4791, Fax:81-42-749-7631)
FEATURES             Location/Qualifiers
     source          1. .37
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                     /db_xref="taxon:9606"
                     /clone="HP00599"
     5'UTR           1. .31
     CDS             32. .>37
                     /codon_start=1
                     /product="ribosomal protein S28"
                     /protein_id="BAB62873.1"
                     /db_xref="GI:15149552"
                     /translation="MD"
BASE COUNT        5 a      19 c       9 g       4 t
ORIGIN


  Query Match             66.0%;  Score 13.2;  DB 9;  Length 37;
  Best Local Similarity   83.3%;  Pred. No. 1.4e+05;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      2 ggaggcgcgacggcagtc 19
          || |||||| |||| |||
Db     28 GGCGGCGCGGCGGCGGTC 11


RESULT  12
I35411/c
LOCUS       I35411          16 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 379 from patent US 5599706.
ACCESSION   I35411
VERSION     I35411.1  GI:2088379
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 379 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
BASE COUNT        2 a      8 c       3 g       3 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 6;  Length 16;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      2 ggaggcgcgacggcag 17
          ||||| ||||| ||||
Db     16 GGAGGTGCGACTGCAG 1


RESULT  13
A04043/c
LOCUS       A04043          23 bp    DNA             PAT       04-JUN-1993
DEFINITION  Synthetic oligonucleotide.
ACCESSION   A04043
VERSION     A04043.1  GI:412381
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   .
  TITLE     tPA-LIKE POLYPEPTIDES, THEIR MANUFACTURE AND USE
  JOURNAL   Patent: WO 9003436-A 13 05-APR-1990;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT        1 a      13 c       5 g       4 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 6;  Length 23;
  Best Local Similarity   87.5%;  Pred. No. 2.4e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 cggaggcgcgacggca 16
          |||||| | |||||||
Db     18 CGGAGGGGAGACGGCA 3


RESULT  14
AR099999
LOCUS       AR099999        50 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 25 from patent US 6080543.
ACCESSION   AR099999
VERSION     AR099999.1  GI:12810447
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Engel,S.R., Descenzo,R.A. and Irelan,N.A.
  TITLE     Detection of fungal pathogens
  JOURNAL   Patent: US 6080543-A 25 27-JUN-2000;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT        9 a      15 c      17 g       9 t
ORIGIN


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  Best Local Similarity   87.5%;  Pred. No. 1.9e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      3 gaggcgcgacggcagt 18
          |||||||| | |||||
Db     12 GAGGCGCGTCCGCAGT 27


RESULT  15
I35351
LOCUS       I35351          52 bp    DNA             PAT       13-MAY-1997
DEFINITION  Sequence 319 from patent US 5599706.
ACCESSION   I35351
VERSION     I35351.1  GI:2088319
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
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  TITLE     Ribozymes targeted to apo(a) mRNA
  JOURNAL   Patent: US 5599706-A 319 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="unknown"
BASE COUNT       16 a     13 c     14 g      9 t
ORIGIN


  Query Match             64.0%;  Score 12.8;  DB 6;  Length 52;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       5 ggcgcgacggcagtcc 20
           |||||||| | |||||
Db       1 GGCGCGACAGAAGTCC 16


Search completed: March 13, 2002, 09:29:13
Job time: 3863 sec
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